

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 3, 2002, 16:22:51 ; Search time 29.94 Seconds  
(without alignments)  
467.445 Million cell updates/sec

Title: US-09-926-256-1  
Perfect score: 699  
Sequence: 1 DLECPGSMYSYDRYCYKPKF.....WFKVDCEDQHSFICKFTRPR 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq.032802.\*  
1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:\*  
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11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:\*  
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13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*  
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15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:\*  
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20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696	99.6	126	AA1979	Snake venom derivate
2	696	99.6	126	AA1981	Snake venom derivate
3	696	99.6	149	AA1981	Snake venom antith
4	696	99.6	149	AA1981	Snake venom derivate
5	696	99.6	149	AA1981	Snake venom derivate
6	696	99.6	149	AA1981	Snake venom derivate
7	348.5	49.9	130	AA1981	Sequence of the pl
8	330.5	47.3	131	AA1981	Sequence of polype
9	330.5	47.3	132	AA1981	Sequence of polype
10	319.5	45.7	133	AA1981	Sequence of polype
11	300.5	43.0	152	AA1981	Snake venom blood

12	265.5	38.0	132	AA1981	Vigera palestinae
13	264.5	37.8	133	AA1981	Sequence of polype
14	255.5	36.6	123	AA1981	Sequence of polype
15	233.5	33.4	127	AA1981	Vigera palestinae
16	222.5	31.8	146	AA1981	Snake venom blood
17	221	31.6	116	AA1981	Sequence of the pl
18	220	31.5	38	AA1981	Snake venom derivate
19	212	30.3	107	AA1981	Sequence of polype
20	209	29.9	36	AA1981	N-terminal sequenc
21	203.5	29.1	125	AA1981	Botrocetin beta su
22	200.5	28.7	125	AA1981	Sequence of polype
23	187	26.8	166	AA1981	Sequence encoded b
24	185	26.5	165	AA1981	Human reg protein.
25	181	25.9	133	AA1981	Human reg protein
26	181	25.9	144	AA1981	Human reg protein
27	181	25.9	146	AA1981	Human reg protein
28	181	25.9	147	AA1981	Reg protein analog
29	181	25.9	166	AA1981	Human reg protein.
30	181	25.9	166	AA1981	Human colon associ
31	181	25.9	166	AA1981	Human cancer associ
32	181	25.9	174	AA1981	Human cancer associ
33	176.5	25.3	175	AA1981	Mouse PAP. Mus mu
34	174	24.9	165	AA1981	MURBG-1. Mus musc
35	172	24.6	44	AA1981	Snake venom derivate
36	171	24.5	50	AA1981	N-terminal sequenc
37	169.5	24.2	175	AA1981	Reg-2 protein. Ra
38	169.5	24.2	175	AA1981	Amino acid sequenc
39	169.5	24.2	175	AA1981	MURBG-2. Mus musc
40	167	23.9	173	AA1981	Mouse PAP. Mus mu
41	166.5	23.8	175	AA1981	Human pancreatilis
42	166.5	23.8	175	AA1981	Human cancer associ
43	166.5	23.8	183	AA1981	Vigera palestinae
44	162	23.2	43	AA1981	Rat reg protein.
45	162	23.2	165	AA1981	

#### ALIGNMENTS

RESULT 1	
ID	AA1979 standard; peptide; 126 AA.
XX	AA1979;
AC	AA1979;
XX	
DT	28-NOV-1995 (first entry)
XX	
DE	Snake venom derived antithrombotic peptide.
XX	
KW	Antithrombotic peptide; snake venom; platelet binding inhibition;
XX	von Willebrand factors; Crocetus horridus horridus.
OS	Crocetus horridus horridus.
XX	
FH	Key
FT	Disulfide-bond 4..15
FT	Disulfide-bond 32..120
FT	Disulfide-bond 95..112
XX	
PN	W09508573-A.
XX	
PD	30-MAR-1995.
XX	
PF	21-SEP-1994; 94WO-JP01555.
XX	
PR	22-SEP-1993; 93JP-0236975.
XX	
PA	(AJTN ) AJTNOMOTO KK.
XX	
PI	Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;
XX	Tanaka A, Yamamoto H, Yoshimoto R;
DR	WPI: 1995-139559/18.

XX Single-chain antithrombotic peptide - obtained by cleaving an  
PT oligopeptide from snake venom to break inter-chain di:sulphide  
PT bonds but preserve intra-chain di:sulphide bonds  
XX  
PS Claim 3; Pages 44-45; 84pp; Japanese.  
XX  
XX AAR71978 and AAR71979 are snake venom derived antithrombotic  
CC peptides, prepared by cleaving the interpeptide but retaining  
CC the intrapeptide disulphide bonds of the original snake venom  
CC oligopeptide. These peptides have the advantage of avoiding  
CC significant thrombocytopenia when administered at the minimum  
CC dose, for in vivo inhibition of platelet von Willebrand factor  
CC binding.  
XX  
XX Sequence 126 AA:  
SQ  
  
Query Match 99.6%; Score 696; DB 16; Length 126;  
Best Local Similarity 99.2%; Pred. No. 3.8e-74;  
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLECPGMSYDRYCYKPFKEQMTWADQRFCSQAKGCHLSVETALEASFYDNLVLAN 60  
Db 1 dlecpqswssydrlycykpfkqemtwaerfcseqakqghllsvetaleasfvdnvllyan 60  
QY 61 KEYLTRYIWIQLRVONKQGPCSSISYENLVDPPECFMWSRDTRLREMFKYDCEQHSFIC 120  
Db 61 keyltrylwiqlrvqnkgpcsslsyenlvdpfecfmwsrtdrlrlewfkydceqhsfic 120  
QY 121 KETRRP 126  
Db 121 ketrpr 126  
  
RESULT 2  
ID AAR71981 standard; Protein; 126 AA.  
XX AAR71981:  
XX AAY85627;  
XX 07-FEB-2001 (first entry)  
XX Snake venom derived protein.  
XX DE  
XX Subunit peptide production; snake venom; rattlesnake; thrombolytic;  
XX von Willebrand's factor; blood platelet-inhibitory activity.  
XX OS  
XX Crotales horridus horridus.  
XX PN  
XX MO20005926-A1.  
XX PD  
XX 12-OCT-2000.  
XX PF  
XX 31-MAR-2000; 2000MO-JP02127.  
XX PR  
XX 02-APR-1999; 99JP-0096073.  
XX PA  
XX (AJIN ) AJINOMOTO CO INC.  
XX PI  
XX Fukuchi N, Kageyama S, Kito M, Kayahara T, Yamamoto H;  
XX WPI; 2000-664985/64.  
XX  
XX Producing physiologically-active subunit peptides originating in  
PT polymer proteins by denaturation and specific separation, with lower  
PT antigenicity but improved solubility and stability, e.g. blood  
PT platelet-binding inhibitors -  
XX  
XX Claim 15; Page 44; 51pp; Japanese.  
XX  
XX This invention relates to a method for the production of a subunit  
CC peptide originating from a polymer protein with disulphide bonds within

CC and between subunits. The method comprises denaturing the protein or its  
CC subunit using a protein denaturing agent in a solution, removing the  
CC agent in the presence of a polyoxalkyl polyether which reacts with a  
CC thiol group and unwinds the subunit, and separating the polyoxalkyl  
CC polyether-bound subunit peptide. The method can be used for producing  
CC physiologically-active subunit peptides for polymer proteins e.g. snake  
CC venom-originated dimer peptide with blood platelet-inhibitory activity  
CC on von Willebrand's factor. The peptides produced have platelet-binding  
CC inhibitory, and thrombolytic activity. The present sequence represents a  
CC rattle snake protein used in an example illustrating the method of the  
XX invention.  
XX  
XX Sequence 126 AA;  
SQ  
  
Query Match 99.6%; Score 696; DB 21; Length 126;  
Best Local Similarity 99.2%; Pred. No. 3.8e-74;  
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DLECPGMSYDRYCYKPFKEQMTWADQRFCSQAKGCHLSVETALEASFYDNLVLAN 60  
Db 1 dlecpqswssydrlycykpfkqemtwaerfcseqakqghllsvetaleasfvdnvllyan 60  
QY 61 KEYLTRYIWIQLRVONKQGPCSSISYENLVDPPECFMWSRDTRLREMFKYDCEQHSFIC 120  
Db 61 keyltrylwiqlrvqnkgpcsslsyenlvdpfecfmwsrtdrlrlewfkydceqhsfic 120  
QY 121 KETRRP 126  
Db 121 ketrpr 126  
  
RESULT 3  
ID AAR71981 standard; Protein; 149 AA.  
XX AAR71981:  
XX AAR71981;  
XX 28-NOV-1995 (first entry)  
XX Snake venom antithrombotic oligopeptide.  
XX DE  
XX Antithrombotic peptide; snake venom; platelet binding inhibition;  
XX von Willebrand factors; Crotales horridus horridus.  
XX OS  
XX Crotales horridus horridus.  
XX FH  
XX Key Location/Qualifiers  
FT Disulfide-bond 27..38  
FT Disulfide-bond 55..143  
FT Disulfide-bond 118..135  
XX PN  
XX MO9508573-A.  
XX PD  
XX 30-MAR-1995.  
XX PF  
XX 21-SEP-1994; 94WO-JP01555.  
XX PR  
XX 22-SEP-1993; 93JP-0236975.  
XX PA  
XX (AJIN ) AJINOMOTO KK.  
XX PI  
XX Fukuchi N, Ishii K, Kito M, Kobayashi T, Nagano M;  
XX Tanaka A, Yamamoto H, Yoshimoto R;  
XX WPI; 1995-139559/18.  
XX N-PSDB; AAO89309.  
XX  
XX Single-chain antithrombotic peptide - obtained by cleaving an  
PT oligopeptide from snake venom to break inter-chain di:sulphide  
PT bonds but preserve intra-chain di:sulphide bonds  
XX  
XX Example 2; Pages 47-48; 84pp; Japanese.



Query Match	Score	DB	Length
Best Local Similarity	96.88	Pred. No. 2e-71	
Matches 122	Conservative	1	Mismatches 3; Indels 0; Gaps
OY	1	DLEPSPGSSSYDRYCYKPKFOEMTWADQRFCSQAKGHLISVETALASPVNDVLYAN	60
Db	1	dlecpsswssdydyrcyprfkqemlwadaerfcscqakgrhlisvetaleasfvndvlyan	60
OY	61	KEYLTRYIWIIGLRVONKGPCSSISYENLVDPCEFWNSRDTRLREWFVKDCQOHSFIC	120
Db	61	keyltrylwglrlqrvnkgpcssisysenlvdpcefcfnvsrdtrtlrewfkvdcqgnsfic	120
OY	121	KFTPRR	126
Db	121	kftpr	126

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RESULT      6
ID          AAR38228
XX
XX          AAR38228 standard; protein, 130 AA.
XX
XX          AAR38228:
XX
DT          01-OCT-1993 (first entry)
XX
DE          Sequence of polypeptide chain of alboaagreggin B1 (AL-B2).
XX
XX          Venom, snake; platelet-binding protein.
XX
XX          Trimeresurus albolabris.
XX
XX          MO9311151-A.
XX
XX          10-JUN-1993.
XX
XX          01-DEC-1992; 92WO-US10344.
XX
XX          03-DEC-1991; 91US-0803630.
XX
XX          05-JUN-1992; 92US-0893929.
XX
XX          (UTEM ) UNIV TEMPLE.
XX
XX          Kirby EP, Peng M;
XX
XX          WPI; 1993-196991/24.
XX
PT          New platelet-binding proteins obtained from snake venom - inhibit
PT          binding of von Willebrand factor to platelet membrane
PT          glycoprotein IB, useful in therapy, diagnosis and surgery
XX
PS          Claim 8; Page 48; 74pp; English.
XX
CC          Alboaagreggin B1 and B2 (collectively "AL-B"), may be obtained in
CC          substantially pure chemical form from venom. Each of AL-B1 and -B2
CC          comprise an about 23 kDa protein formed by an about 17 kDa
CC          polypeptide chain crosslinked to an about 14 kDa polypeptide chain
CC          by one or more interchain disulfide bonds. Each of the two
CC          polypeptide chains of AL-B1 and -B2 show strong homology to two of
CC          the chains of AL-A. AL-B1 and -B2 each comprise two non-identical
CC          polypeptide chains.
XX
XX          Sequence 130 AA;
XX
Query Match 49.9%; Score 348.5; DB 14; Length 130;
Best Local Similarity 50.8%; Pred. No. 3.8e-33;
Matches 66; Conservative 24; Mismatches 27; Indels 13; Gaps
3
3 ECPSGMSYSDRYCKRPFQEQETWADQAFRCSEQAQAGHLSYETALEASFVDMVLYAN-K 61
1 dcpdwsafkgycygylvkektwedaerfcsegandqhlvsyreavfaellsenvk 60

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QY 62 EXLRYYTWIGLRVYKNGKQPC-----SISYEMLV--DPECPMVRDRLRLRMFVYDC 112
Db 61 ky--hwvlllsvqvkqgqcssewsdgssvsyenlvxnpnkcvtvlkkesefkctwsnyc 117
QY 113 EOOHSFICKF 122
Db 118 eqkhlfmckf 127
```

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RESULT      7
AAR88222    AAR88222 standard; protein. 131 AA.
XX          AAR88222;
AC          AAR88222;
XX          AAR88222;
DT          01-OCT-1993   (first entry)
XX          Sequence of polypeptide chain of alboaaggreglin A (Al-A).
DE          Sequence of polypeptide chain of platelet-binding protein.
KM          Venom; snake; platelet-binding protein.
OS          Trimeresurus albolabris.
XX          WO9311151-A.
PN          10-JUN-1993.
PD          01-DEC-1992;   92WO-US10344.
PF          03-DEC-1991;   91US-0803630.
PR          05-JUN-1992;   92US-0893929.
FA          (UTEM ) UNIV TEMPLE.
XX          Kirby EP, Peng M;
PI          WPI; 1993-196991/24.
DR          New platelet-binding proteins obtained from snake venom - inhibit
PT          binding of von Willebrand factor to platelet membrane
SP          glycoprotein IB, useful in therapy, diagnosis and surgery
XX          Claim 4; Page 45; 74pp; English.
PS          Al-A may be obt'd. from snake venom. It has a mol. wt. of about 45
XX          kDa. Al-A contains two types of polypeptide chains, with mol. wt.. of
CC          about 18 kDa and about 15 kDa, respectively. Each of these two types
CC          of chains is actually composed of two subtypes. Thus, Al-A comprises
CC          four non-identical polypeptide chains. A possible variation of
CC          AAR88224 has been found, characterised by Asp at posn. three in lieu
CC          of Cys.
XX          Sequence     131 AA;
SQ          Query Match           47.3%; Score 330.5; DB 14; Length 131;
Best Local Similarity 45.8%; Pred.No. 5,1e-31;
Matches 60; Conservative 23; Mismatches 39; Indels 9; Gaps 2;
OY       3 ECPSSGMSSTDYRCRYCFPEQEMTWADAORFCRQAAGCHLSVETALASFYVNVLKANKE 62
        :| | | |||||:||::| | |||||:|| |||||:|| | ::|
Db       1 dcpdswssydyqcyvfkrlqltwedaericsgqandghlvsiesagdadfvqlvsenlr 60
        :| | | |||||:||::| | |||||:|| |||||:|| | ::|
OY       63 YLTRITWIGLRNONGQP-----SISYEHLVD--PFECEFNVSRPDRLREMPKVDCE 113
        :| | | |||||:|| | | | | | | | | | | | | | | | | 
Db       61 sekhyvvwglrtvgsggcsewsdgssvhwmlgleknlrkkyglekraeftwnvyvcg 120
        : : | | | | |
OY       114 QQHSEFCKPTR 124
        : : | | | | |
Db       121 heyflevckfxkr 131

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PR 05-JUN-1992; 92US-0893929.  
XX (UTEM ) UNITV TEMPLE.  
XX Kirby BP, Peng M;  
XX WPI: 1993-196991/24.  
DR New platelet-binding proteins obtained from snake venom - inhibit  
PT binding of von Willebrand factor to platelet membrane  
PT glycoprotein IB, useful in therapy, diagnosis and surgery  
PS Claim 4; Page 46; 74pp; English.  
XX AL-A may be obt'd. from snake venom. It has a mol. wt. of about 45  
CC kDa. AL-A contains two types of polypeptide chains, with mol. wt. of  
CC about 18 kDa and about 15 kDa, respectively. Each of these two types  
CC of chains is actually composed of two subtypes. Thus, AL-A comprises  
CC four non-identical polypeptide chains. A possible variation of  
CC AAR38224 has been found, characterised by Asp at posn. three in lieu  
CC of Cys.  
CC  
CC  
SQ Sequence 134 AA;  
  
Query Match 45.7%; Score 319.5; DB 14; Length 134;  
Best Local Similarity 42.7%; Pred. No. 1e-29; Mismatches 39; Indels 9; Gaps 2;  
Matches 56; Conservative 27;  
  
QY 1 DLECPGSSSYDRYCYRPFKQEMTWADQRFCSQAKGHLISVETALASFYDNLVYAN 60  
DB 1 dfhclpgwsayddqcyvfnepknwedeerfcakqadsghlvsleimgaadvayqlisen 60  
QY 61 KEVLTFTWIGLRVQNGQPC-----SSISYENLVDPFE--ECFVNSRDTLRLEWFKVD 111  
DB 61 lqskenhvwwlglkvqkqcgsssgsvlyenllklmktcgaleqsgfirkwlnlg 120  
QY 112 CEOQHSFICKF 122  
DB 121 clqlnplfvckf 131  
  
RESULT 11  
AAM51543  
ID AAM51543 standard; Protein: 152 AA.  
XX  
AC AAM51543;  
XX  
DT 10-JAN-2002 (first entry)  
XX  
DE Snake venom blood anticoagulant halysin A chain.  
XX  
KW Snake; pit viper; venom; halysin; anticoagulant; thrombogenesis;  
KM thrombosis.  
XX  
OS Agkistrodon halys.  
XX  
PN KR2001049671-A.  
XX  
PD 15-JUN-2001.  
XX  
PF 29-JUN-2000; 2000KR-0036591.  
XX  
PR 29-JUN-1999; 99KR-0025105.  
XX  
PA (BIOB-) BIOBUD CO LTD.  
XX  
PI Jang YS, Jung GH, Kim DS, Koo BH, Son YD;  
XX WPI: 2001-637330/73.  
XX N-PSDB; AAI71876.  
XX  
PT Halysin as blood anticoagulation protein separated from snake venom -

XX  
PS Claim 2; Page 10; 21pp; Korean.  
XX  
CC The invention relates to halysin, a novel protein with very strong  
CC blood anticoagulation activity. The protein was separated from snake  
CC venom of Agkistrodon halys brevicaudus (a Korean pit viper) and can  
CC be used in the treatment of thrombogenesis. The present sequence  
CC is the A chain of halysin.  
XX  
SQ Sequence 152 AA;  
  
Query Match 43.0%; Score 300.5; DB 22; Length 152;  
Best Local Similarity 41.4%; Pred. No. 2.2e-27;  
Matches 53; Conservative 29; Mismatches 37; Indels 9; Gaps 2;  
  
QY 3 ECPGSSSYDRYCYRPFKQEMTWADQRFCSQAKGHLISVETALASFYDNLVYANKE 62  
DB 24 dcpqswssyeghcnlfnlftkwaeeerfcrkqkghlvslesseadvayqlvsemnk 83  
QY 63 YLTRYTWIGLRVQNGQPC-----SSISYENLVDPFE--CFVNSRDTLRLEWFKVDCE 113  
DB 84 rygllywlgilvrgkkgcgssqsgsvsygnwieaasktcglqketeirkwfnlycg 143  
QY 114 QQHSFICK 121  
DB 144 ernpfvce 151  
  
RESULT 12  
ID AAR72235 standard; peptide: 132 AA.  
XX  
AC AAR72235;  
XX  
DT 04-DEC-1995 (first entry)  
XX  
DE Vipera palestinae venom derived peptide.  
XX  
KW Vipera palestinae; venom; antithrombotic agent;  
KM platelet binding; von Willebrand factor.  
XX  
OS Vipera palestinae.  
XX  
PN W09509183-A.  
XX  
PD 06-APR-1995.  
XX  
PF 27-SEP-1994; 94WO-JP01583.  
XX  
PR 28-SEP-1993; 93JP-0241666.  
PR 14-JAN-1994; 94JP-0002691.  
PR 10-JUN-1994; 94JP-0128518.  
XX  
PA (AJIN ) AJINOMOTO KK.  
XX  
PI Fukuchi N, Ishii K, Kaida K, Kobayashi T;  
XX WPI: 1995-147392/19.  
XX  
PT Peptide derived from Vipera palestinae venom - inhibits binding  
PT of platelets to von Willebrand factor, useful as antithrombotic  
PT agent  
PS Claim 5; Page 19; 37pp; Japanese.  
XX  
CC AAR72235 is a Vipera palestinae venom derived peptide. A peptide  
CC compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the  
CC binding of platelets to von Willebrand factors and can therefore  
CC be used as an anti- thrombotic agent.  
XX  
SQ Sequence 132 AA;

	Query Match	38.0%;	Score 265.5;	DB 16;	Length 132;
	Best Local Similarity	39.1%;	Pred. No. 2.4e-23;		
	Matches 50;	Conservative 25;	Mismatches 46;	Indels 7;	Gaps 1;
OY	1 DLECSGMSVDRYCYKPFKOEMTADAOFCSEQAKGGHLSVETALEASFDVNYLAN 60				
Db	1 dgdcdpsdssshnegchcykfrlftkweeakfcmqyngmwhlasiesveeanltvaelsvkt 60				
OY	61 KEYLTRIYWIGLRVNKGQPCSS-----ISYENLVDFECCFMWSRDTRLREMFKVDC 113				
Db	61 llskxyhawigjrdsergqscshvdsgsavseyelvtckcfjgnkdxylewltlpce 120				
OY	114 QQHSPICK 121				
Db	121 dkipflck 128				
	RESULT 13				
ID	AAR38230				
XX	AAR38230 standard; protein; 133 AA.				
AC	AAR38230;				
XX	01-OCT-1993 (first entry)				
DT	Sequence of polypeptide chain of alboaagregrin-like protein called				
XX	echnicetin.				
DE	Venom; snake; platelet-binding protein.				
XX	Echis carinatus.				
OS	W09311151-A.				
FN	10-JUN-1993.				
PD	01-DEC-1992; 92MO-US10344.				
PE	03-DEC-1991; 91US-0803630.				
PR	05-JUN-1992; 92US-0893929.				
XX	(UTEM ) UNIV TEMPLE.				
PA	Kirby EP, Peng M;				
PI	WPI; 1993-196991/24.				
DR	New platelet-binding proteins obtained from snake venom - inhibit				
XX	* binding of von Willebrand factor to platelet membrane				
PT	glycoprotein IB, useful in therapy, diagnosis and surgery				
PS	Claim 10; Page 49; 74pp; English.				
XX	Echinacin, is obtained in substantially pure chemical form from				
CC	venom, as an about 26 kDa protein which likely comprises a dimer				
CC	composed of two types of chains. One chain type has a mol. wt. of				
CC	about 15 kDa and the other has a mol. wt. of about 13 kDa. The				
CC	individual polypeptide chains are held together by one or more				
CC	interchain disulfide bonds.				
XX	Sequence 133 AA;				
OY	Query Match	37.8%;	Score 264.5;	DB 14;	Length 133;
	Best Local Similarity	37.8%;	Pred. No. 3.2e-23;		
	Matches 51;	Conservative 32;	Mismatches 41;	Indels 11;	Gaps 4;
OY	1 DLECSGMSVDRYCYKPFKOEMTADAOFCSEQAKGGHLSVETALEASFDVNYLAN 60				
Db	1 dgdcdsjsfyeghegyqlfrlk-twdeaeekycn-qwdsgghlvstiesnakaetvraqllsrk 58				
OY	61 --KEYLTRIYWIGLRVNKGQPC-----SSISYENLVDFECCFMWSRDTRLREMFKYD 111				

Dd		59	lpksiedrwtwlgldrdkrregcglnhwcdnstvhyehvpptckvtlertqefirwianv	118
OY		112	CEQOHSFTCKFTRPR	126
Dd		119	cefkpfvcyakipr	133
<hr/>				
RESULT 14				
ID	AAR38225	standard; protein; 123 AA.		
AC	AAR38225;			
DT	01-OCT-1993	(first entry)		
DE	Sequence of polypeptide chain of alboaagreglin A (AL-A).			
KW	Venom; snake; platelet-binding protein.			
OS	Trimeresurus albolabris.			
PN	W09311151-A.			
PD	10-JUN-1993.			
PF	01-DEC-1992;	92WO-US10344.		
PR	03-DEC-1991;	91US-0803630.		
PR	05-JUN-1992;	92US-0893929.		
PA	(UTEM ) UNIV TEMPLE.			
PI	Kirby EP, Peng M;			
DR	WPI: 1993-196991/24.			
XX				
PT	New platelet-binding proteins obtained from snake venom - inhibit			
PT	binding of von Willebrand factor to platelet membrane			
PT	glycoprotein IB, useful in therapy, diagnosis and surgery			
PS	Claim 4; Page 47; 7app; English.			
CC	Al-A may be obt'd. from snake venom. It has a mol. wt. of about 45			
CC	kDa. Al-A contains two types of polypeptide chains, with mol. wt. of			
CC	about 18 kDa and about 15 kDa, respectively. Each of these two types			
CC	of chains is actually composed of two subtypes. Thus, Al-A comprises			
CC	four non-identical polypeptide chains. A possible variation of			
CC	AAR38224 has been found, characterised by asp at posn. three in lieu			
CC	of Cys.			
XX				
SQ	Sequence	123 AA;		
<hr/>				
OQuery Match		36.6%;	Score 255.5;	DB.14; Length 123;
Best Local Similarity		39.7%;	Pred. No.3.3e-22;	
Matches 52;	Conservative	23;	Mismatches 35;	Indels 21; Gaps 6;
OY	3 BCPSSMSVDRYCYKPKFOEWTADQRFCSEDAKGHLSTETALEAFVDN---	VLY 58		
Dd	:         :      :	:           :   :		
	1 depdsawsyeghcyyvfnepqmwadaekfctgqhghslstsfsgsgadfvvmqrplln	60		
OY	59 ANKEVLTRYITWGLRNVQNGQPCCS-----ISTENLVDPPECFWRSRDRLRKREFKVD	111		
Dd	:      :	:  :		
	61 an-----lwlygl--snlwmcusqwsdgtxldyxwreqfec-lvarltln-newlsmd	110		
OY	112 CEQOHSFTCKF	122		
Dd	:   :			
	111 cssthsvcef	121		
<hr/>				
RESULT 15				
AAR72236				

```

ID AAR72236 standard; peptide: 127 AA.
XX
AC AAR72236;
XX
DT 04-DEC-1995 (first entry)
XX
DE Vipera palestinae venom derived peptide.
XX
KW Vipera palestinae; venom; antithrombotic agent;
XX platelet binding; von Willebrand factor.
OS Vipera palestinae.
XX
PN WO9509183-A.
XX
PD 06-APR-1995.
XX
PF 27-SEP-1994; 94MO-JP01583.
XX
PR 28-SEP-1993; 93JP-0241666.
PR 14-JAN-1994; 94JP-0002691.
PR 10-JUN-1994; 94JP-0128518.
XX
PA (AJTN ) AJINOMOTO KK.
XX
PI Fukuchi N, Ishii K, Kaide K, Kobayashi T;
XX
DR WPI; 1995-147392/19.
XX
PT Peptide derived from Vipera palestinae venom - inhibits binding
PT of platelets to von Willebrand factor, useful as antithrombotic
PT agent
XX
PS Claim 5; Pages 19-20; 37pp; Japanese.
XX
CC AAR72236 is a Vipera palestinae venom derived peptide. A peptide
CC compsn. comprising AAR72235 and AAR72236 is claimed, it inhibits the
CC binding of platelets to von Willebrand factors and can therefore
CC be used as an anti- thrombotic agent.
XX
SQ Sequence 127 AA;

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Query Match 33.4%; Score 233.5; DB 16; Length 127;
Best Local Similarity 36.6%; Pred. No. 1.4e-19;
Matches 48; Conservative 25; Mismatches 45; Indels 13; Gaps 4;

OY 3 ECPSCGSSVDRVCYKPFKQETWADQPCSEOAQKCHLSVETALEASFVNVLYANKE 62
DB 1 dcpsdwsshegncykvinidtwadaekfctegvsgghlslskstevdfmklivipilk 60
OY 63 YLTRYIMIGLRVONKGGPCS-----SISYENLVDPFECFVSRDTRLREWFKYDCEQ 115
DB 61 y--dlwlgf--snfwrclmngwsgvkllykavsdipdcyvak--twdygwllrdcst 114
OY 116 HSFICKFTPR 126
DB 115 ykfickrvpr 125

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Search completed: October 3, 2002, 16:24:50  
Job time: 119 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 16:23:06 ; Search time 12.89 Seconds  
(without alignments)  
238.761 Million cell updates/sec

Title: US-09-926-256-1

Perfect score: 699  
Sequence: 1 DLECPGSGWSSYDRYCKPKF.....WFKVDEQGHSTCKTTPR 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PC105.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfill1st.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	696	99.6	126	2	US-08-612-840A-2
2	696	99.6	149	2	US-08-612-840A-8
3	673	96.3	127	1	US-07-614-443A-1
4	673	96.3	127	1	US-08-294-859-1
5	673	96.3	127	1	US-08-481-676-1
6	348.5	49.9	130	1	US-07-893-929A-7
7	348.5	49.9	130	5	PCT-US92-10344-7
8	338.5	48.4	131	1	US-07-893-929A-1
9	338.5	48.4	131	5	PCT-US92-10344-1
10	333.5	47.7	132	1	US-07-893-929A-5
11	333.5	47.7	132	5	PCT-US92-10344-5
12	319.5	45.7	134	5	US-07-893-929A-2
13	319.5	45.7	134	5	PCT-US92-10344-2
14	264.5	37.8	133	1	US-07-893-929A-9
15	264.5	37.8	133	5	PCT-US92-10344-9
16	263.5	37.7	123	1	US-07-893-929A-4
17	263.5	37.7	123	5	PCT-US92-10344-4
18	223.5	32.0	117	1	US-07-614-443A-2
19	223.5	32.0	117	1	US-08-294-859-2
20	223.5	32.0	117	1	US-08-481-676-2
21	220	31.5	38	2	US-08-612-840A-1
22	212	30.3	107	5	US-07-893-929A-6
23	212	30.3	107	5	PCT-US92-10344-6
24	200.5	28.7	125	1	US-07-893-929A-3
25	200.5	28.7	125	1	PCT-US92-10344-3
26	174.5	25.0	175	2	US-08-401-530A-3
27	174.5	25.0	175	2	US-08-709-662-3

28	171	24.5	50	1	US-07-614-443A-5	Sequence 5, Appl1
29	171	24.5	50	1	US-08-294-859-5	Sequence 5, Appl1
30	171	24.5	50	1	US-08-481-676-5	Sequence 10, Appl1
31	170	24.3	123	1	US-07-893-929A-10	Sequence 10, Appl1
32	170	24.3	123	5	PCT-US92-10344-10	Sequence 10, Appl1
33	166.5	23.8	175	2	US-08-464-637-2	Sequence 2, Appl1
34	166.5	23.8	175	2	US-08-401-530A-4	Sequence 4, Appl1
35	166.5	23.8	175	2	US-08-709-662-4	Sequence 4, Appl1
36	166.5	23.8	175	2	US-08-822-261-3	Sequence 4, Appl1
37	161.5	23.1	175	2	US-08-822-261-1	Sequence 1, Appl1
38	160.5	23.0	128	1	US-07-893-929A-8	Sequence 8, Appl1
39	160.5	23.0	128	5	PCT-US92-10344-8	Sequence 8, Appl1
40	160	22.9	165	2	US-08-401-530A-7	Sequence 7, Appl1
41	160	22.9	165	2	US-08-729-103-3	Sequence 3, Appl1
42	160	22.9	165	2	US-08-709-662-7	Sequence 7, Appl1
43	160	22.9	166	2	US-08-729-103-4	Sequence 4, Appl1
44	155.5	22.2	174	1	US-07-778-156-7	Sequence 7, Appl1
45	155.5	22.2	174	2	US-08-822-261-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-08-612-840A-2  
; Sequence 2, Application US/08612840A  
; Patent No. 5856126  
; GENERAL INFORMATION:  
; APPLICANT: FUKUCHI, Naoyuki  
; APPLICANT: YAMAMOTO, Hiroshi  
; APPLICANT: NAGANO, Mitsuyo  
; APPLICANT: KITAO, Morikazu  
; APPLICANT: TANAKA, Akiko  
; APPLICANT: ISHII, Koichi  
; APPLICANT: KOBAYASHI, Tsuyoshi  
; APPLICANT: YOSHIMOTO, Ryota  
; TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND  
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Obion, Spivak, McClelland, Maier & Neustadt, P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,840A  
; FILING DATE: 20-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-236975  
; FILING DATE: 22-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5856126man F. Obion  
; REGISTRATION NUMBER: 24,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 126 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-612-840A-2

Query Match 99.6%; Score 696; DB 2; Length 126;  
Best Local Similarity 99.2%; Pred. No. 7.7e-79;  
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEQAKGHLSTVTALEASFVNVLYAN 60  
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DB 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEQAKGHLSTVTALEASFVNVLYAN 60  
|||||

QY 61 KEYLTRYIWLGLRVONKQPCSSISENLVDPFECFVNSRDTRLREMFVKVDCQOHSFIC 120  
|||||  
DB 61 KEYLTRYIWLGLRVONKQPCSSISENLVDPFECFVNSRDTRLREMFVKVDCQOHSFIC 120  
|||||

QY 121 KETRRP 126  
|||||  
DB 121 KETRRP 126

RESULT 2  
US-08-612-840A-8  
; Sequence 8, Application US/08612840A  
; Patent No. 5856126  
; GENERAL INFORMATION:  
; APPLICANT: FUKUCHI, Naoyuki  
; APPLICANT: YAMAMOTO, Hiroshi  
; APPLICANT: NAGANO, Mitsuyo  
; APPLICANT: KITO, Morikazu  
; APPLICANT: TANAKA, Akiko  
; APPLICANT: ISHII, Koichi  
; APPLICANT: KOBAYASHI, Tsuyoshi  
; APPLICANT: YOSHIMOTO, Ryota  
; TITLE OF INVENTION: PEPTIDE HAVING ANTI-THROMBUS ACTIVITY AND  
; TITLE OF INVENTION: METHOD OF PRODUCING THE SAME  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/612,840A  
; FILING DATE: 20-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5-236975  
; FILING DATE: 22-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5856126man F. Oblon  
; REGISTRATION NUMBER: 24,618  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 149 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-612-840A-8

Query Match 99.6%; Score 696; DB 2; Length 149;  
Best Local Similarity 99.2%; Pred. No. 9.7e-79;  
Matches 125; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEQAKGHLSTVTALEASFVNVLYAN 60  
|||||

DB 24 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEQAKGHLSTVTALEASFVNVLYAN 83  
QY 61 KEYLTRYIWLGLRVONKQPCSSISENLVDPFECFVNSRDTRLREMFVKVDCQOHSFIC 120  
|||||  
DB 84 KEYLTRYIWLGLRVONKQPCSSISENLVDPFECFVNSRDTRLREMFVKVDCQOHSFIC 143  
QY 121 KETRRP 126  
|||||  
DB 144 KETRRP 149

RESULT 3  
US-07-614-443A-1  
; Sequence 1, Application US/07614443A  
; Patent No. 5342830  
; GENERAL INFORMATION:  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/614,443A  
; FILING DATE: 19901116  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22803-20003.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-614-443A-1

Query Match 96.3%; Score 673; DB 1; Length 127;  
Best Local Similarity 96.8%; Pred. No. 5.6e-76;  
Matches 122; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEQAKGHLSTVTALEASFVNVLYAN 60  
|||||  
DB 1 DLECPGWSYDRYCYKPFKQEMTWADAFRCSEQAKGHLSTVTALEASFVNVLYAN 60  
|||||

QY 61 KEYLTRYIWLGLRVONKQPCSSISENLVDPFECFVNSRDTRLREMFVKVDCQOHSFIC 120  
|||||  
DB 61 KEYLTRYIWLGLRVONKQPCSSISENLVDPFECFVNSRDTRLREMFVKVDCQOHSFIC 120  
|||||

QY 121 KETRRP 126  
|||||  
DB 121 KETRRP 126

RESULT 4  
US-08-294-859-1  
; Sequence 1, Application US/08294859  
; Patent No. 5679542

1. GENERAL INFORMATION:  
 2. APPLICANT: SCARBOROUGH, ROBERT M.  
 3. TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS  
 4. NUMBER OF SEQUENCES: 7  
 5. CORRESPONDENCE ADDRESS:  
 6. ADDRESSEE: Morrison & Foerster  
 7. STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
 8. CITY: Washington, D.C.  
 9. COUNTRY: USA  
 10. ZIP: 20006-1888  
 11. COMPUTER READABLE FORM:  
 12. MEDIUM TYPE: Floppy disk  
 13. COMPUTER: IBM PC compatible  
 14. OPERATING SYSTEM: PC-DOS/MS-DOS  
 15. SOFTWARE: PatentIn Release #1.0, Version #1.25  
 16. CURRENT APPLICATION DATA:  
 17. APPLICATION NUMBER: US/08/294,859  
 18. FILING DATE: 29-AUG-1994  
 19. CLASSIFICATION: 435  
 20. ATTORNEY/AGENT INFORMATION:  
 21. NAME: Murashige, Kate H.  
 22. REGISTRATION NUMBER: 29,959  
 23. REFERENCE/DOCKET NUMBER: 2803-0003.10  
 24. TELECOMMUNICATION INFORMATION:  
 25. TELEPHONE: (202) 887-1500  
 26. TELEFAX: (202) 887-0763  
 27. TELEX: 904030  
 28. INFORMATION FOR SEQ ID NO: 1:  
 29. SEQUENCE CHARACTERISTICS:  
 30. LENGTH: 127 amino acids  
 31. TYPE: amino acid  
 32. STRANDEDNESS: single  
 33. TOPOLOGY: linear  
 34. IS-08-294-859-1

Query Match	96.3%;	Score 673;	DB 1;	Length 127;
Best Local Similarly	96.8%;	Pred. No. 5.6e-76;		
Matches 122; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0

Qy	1	DLECPGSSGSSYDRCYCRKPEKREMTMAADORAECSSQAGHLLSVETLLEASFVNDVLYAN	60
Db	1	DLECPGSSGSSYDRCYCRKPEKREMTMAADORAECSSQAGHLLSVETLLEASFVNDVLYAN	60
Qy	61	KEYLRYRWIWLRYONKNGQPSSISYENLVDPECFMWSBDTRLREKFKYDCQOHSFTC	120
Db	61	KEYLRYRWIWLRYONKNGQPSSISYENLVDPECFMWSBDTRLREKFKYDCQOHSFTC	120
Qy	121	KETRRP	126
Db	121	KETRRP	126

RESULT 5  
US-08-481-676-1  
: Sequence 1, Application US/08481676  
: Patent No. 5744584  
: GENERAL INFORMATION:  
: APPLICANT: SCARBOROUGH, ROBERT M.  
: TITLE OF INVENTION: ANTI-THROMBOSIS AGENTS  
: NUMBER OF SEQUENCES: 7  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Morrison & Foerster  
: STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
: CITY: Washington, D.C.  
: COUNTRY: USA  
: ZIP: 20006-1888  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,676  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/294,859  
 FILING DATE: 29-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Murashige, Kate H.  
 REGISTRATION NUMBER: 29,959  
 REFERENCE/DOCKET NUMBER: 2803-0003.10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 887-1500  
 TELEFAX: (202) 887-0763  
 TELEX: 90-4030  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 127 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-08-481-676-1

Query Match	96.38;	Score 673;	DB 1;	Length 127;
Best Local Similarity	-96.88;	Pred. No. 5.6e-76;		
Matches 122; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;

[illegible]

QY	121	KFTTRPR	126
Db	121	KFTTRPR	126

RESULT 6  
US-07-893-

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:
:   REGISTRATION NUMBER: 30,480
:   REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
:   TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (215) 568-8383
:   TELEFAX: (215) 568-5549
:   TELEX: No. 5336667e
:   INFORMATION FOR SEQ ID NO: 7:
:   SEQUENCE CHARACTERISTICS:
:   LENGTH: 130 amino acids
:   TYPE: AMINO ACID
:   TOPOLOGY: linear
:
US-07-893-929A-7

Query Match
Best Local Similarity 49.9%; Score 348.5; DB 1; Length 130;
Matches 66; Conservative 24; Mismatches 27; Indels 13; Gaps 4;

QY 3 ECPGWSYDRYCYKPFQEMTWADQRFCSQAKGGHLLSVETALASFDVNLVYAN-K 61
: ||| ||| : ||| : ||| ||| ||| : ||| : ||| : |||
Db 1 DCPDWSFFKQCYQIVYELKTWEDAEFCSEQANDGHLVSIESYREAVFVALLSENVK 60
QY 62 EYLRITWIGLRVQNKGPC-----SSISYENLV--DPECFMVSRDTRLREMFKVC 112
: | : ||| ||| ||| ||| ||| ||| ||| : ||| : ||| : |||
Db 61 KY--HWIGLSYVQNKGGQCSSEWSDSSVYENLVKPNPKCFVLKKESEFKTWSNVYC 117
QY 113 EQHSHFICK 122
: ||| : |||
Db 118 EQKHIFMCKF 127

RESULT 7
PCT-US92-10344-7
: Sequence 7, Application PC/TUS9210344
: GENERAL INFORMATION:
: APPLICANT: Kirby, Edward P.
: TITLE OF INVENTION: Alboaggregins: Platelet
: TITLE OF INVENTION: Agonists which bind to Platelet
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Temple University - Of The Common-
: STREET: 406 University Services Building
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: U.S.A.
: ZIP: 19122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/10344
: FILING DATE: 19921201
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/803,630
: FILING DATE: December 3, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Monaco, Daniel A.
: REGISTRATION NUMBER: 30,480
: REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-8383
: TELEFAX: (215) 568-5549
: TELEX: None
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 130 amino acids
: TYPE: AMINO ACID

```

```

:   TOPOLOGY: linear
:
PCT-US92-10344-7

Query Match
Best Local Similarity 49.9%; Score 348.5; DB 5; Length 130;
Matches 66; Conservative 24; Mismatches 27; Indels 13; Gaps 4;

QY 3 ECPGWSYDRYCYKPFQEMTWADQRFCSQAKGGHLLSVETALASFDVNLVYAN-K 61
: ||| ||| : ||| : ||| ||| ||| : ||| : ||| : |||
Db 1 DCPDWSFFKQCYQIVYELKTWEDAEFCSEQANDGHLVSIESYREAVFVALLSENVK 60
QY 62 EYLRITWIGLRVQNKGPC-----SSISYENLV--DPECFMVSRDTRLREMFKVC 112
: | : ||| ||| ||| ||| ||| ||| ||| : ||| : ||| : |||
Db 61 KY--HWIGLSYVQNKGGQCSSEWSDSSVYENLVKPNPKCFVLKKESEFKTWSNVYC 117
QY 113 EQHSHFICK 122
: ||| : |||
Db 118 EQKHIFMCKF 127

RESULT 8
US-07-893-929A-1
: Sequence 1, Application US/07893929A
: Patent No. 5336667
: GENERAL INFORMATION:
: APPLICANT: Kirby, Edward P.
: TITLE OF INVENTION: Alboaggregins: Platelet
: TITLE OF INVENTION: Agonists which bind to Platelet
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Temple University - Of The Common-
: STREET: 406 University Services Building
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: U.S.A.
: ZIP: 19122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/893,929A
: FILING DATE: 19920605
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/803,630
: FILING DATE: December 3, 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Monaco, Daniel A.
: REGISTRATION NUMBER: 30,480
: REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-8383
: TELEFAX: (215) 568-5549
: TELEX: No. 5336667e
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 131 amino acids
: TYPE: AMINO ACID
: .TOPOLOGY: linear
:
US-07-893-929A-1

Query Match
Best Local Similarity 48.4%; Score 338.5; DB 1; Length 131;
Matches 62; Conservative 21; Mismatches 39; Indels 9; Gaps 2;

QY 3 ECPGWSYDRYCYKPFQEMTWADQRFCSQAKGGHLLSVETALASFDVNLVYANKE 62

```



TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESS: wealth System of Higher Education  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10344  
FILING DATE: 19921201  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
PCT-US92-10344-5

Query Match 47.7%; Score 333.5; DB 5; Length 132;  
Best Local Similarity 47.3%; Pred. No. 7,6e-34;  
Matches 61; Conservative 24; Mismatches 35; Indels 9; Gaps 2;

QY 3 ECPSSGWSYDRYCYKPKQEMTADARFCSEQAKGGHLSVETALASFPDNLVYANKE 62  
DB 1 DCPSPDSSFKQCYQYKELKEDAEKFCSEQANDGHLVSIESYREAVFVALLSENVK 60

QY 63 YLTRYTWIGLRVONKQGPC-----SSISYENLV--DPFCFMYSRPTRLREMFVDC 113  
DB 61 TTKYVWIGLSVONKQDCSEMSDSSSVYENLIKRPKRCFVLKKESEFTWSNVYCE 120

QY 114 QOHSFICKF 122  
DB 121 QKHFWCKF 129

RESULT 12  
US-07-893-929A-2  
Sequence 2, Application US/07893929A  
Patent No. 5336667  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
TITLE OF INVENTION: Alboaggregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESS: wealth System of Higher Education  
CITY: Philadelphia  
STATE: Pennsylvania

COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/893,929A  
FILING DATE: 19920605  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 07/803,630  
FILING DATE: December 3, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-126 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5336667e  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 134 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
US-07-893-929A-2

Query Match 45.7%; Score 319.5; DB 1; Length 134;  
Best Local Similarity 42.7%; Pred. No. 4,2e-32;  
Matches 56; Conservative 27; Mismatches 39; Indels 9; Gaps 2;

QY 1 DLECPSSGWSYDRYCYKPKQEMTADARFCSEQAKGGHLSVETALASFPDNLVYAN 60  
DB 1 DFHCLPGMSAYDYCYKPFNEPKNMDAERFCQKQDSGHLVSIETMGDAFVAQLISEN 60

QY 61 KEYLTRYTWIGLRVONKQGPC-----SSISYENLVDPF--ECFMYSRPTRLREMFV 111  
DB 61 IOSNEHYWIGLRVONKQDCSEMSDSSSVYENLIKRMKRCALDSEGRKRWNLG 120

QY 112 CEQOHSFICKF 122  
DB 121 CIQLNPFVCKF 131

RESULT 13  
PCT-US92-10344-2  
Sequence 2, Application PC/TUS9210344  
GENERAL INFORMATION:  
APPLICANT: Kirby, Edward P.  
TITLE OF INVENTION: Alboaggregins: Platelet  
TITLE OF INVENTION: Agonists Which Bind To Platelet  
TITLE OF INVENTION: Membrane Glycoprotein Ib  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESS: wealth System of Higher Education  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/10344  
FILING DATE: 19921201



Query Match 37.8%; Score 264.5; DB 5; Length 133;  
Best Local Similarity 37.8%; Pred. No. 2.8e-25;  
Matches 51; Conservative 32; Mismatches 41; Indels 11; Gaps 4;  
QY 1 DLECPGWSSTDRYCYKPPKQEMTWADAORFCSEAKGHLLSVETALEASPVNDVLIYAN 60  
| : | | | | : : | | : : | | | | : : | | : :  
Db 1 DODCLSGMSFEGHCYQLFLK-TWDEAEKYN-OWDGGHLVIESNAKAEFVAQLISRK 58  
QY 61 --KEYLRYTWIGLRVONKQPC-----SSISYENLVDPFCEMVSRDTRLREMFKVD 111  
| : | | | | : : | | : : | | : : | | : : | | : :  
Db 59 LPKSAIEDRWIGLDRSKRECGHLMTDNSFVHEHVPPTKCFVLERQTERFERKWIAYN 118  
QY 112 CEOQHSFICKFTRRP 126  
| : | : | : | |  
Db 119 CEFEKPFVCKAKIPR 133

Search completed: October 3, 2002, 16:25:09  
Job time: 123 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2002, 16:23:36 ; Search time 16.24 Seconds

(without alignments)  
745,521 Million cell updates/sec

Title: US-09-926-256-1

Perfect score: 699

Sequence: 1 DLECPGSMSSYDRYCKYKPKF.....WPKYDCEQHSEICKFTPRR 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	344.5	49.3	129	2 JC4329	coagulation factor
2	323	46.2	133	2 A47267	botrocetin alpha c
3	314.5	45.0	152	2 JC4690	coagulation factor
4	303.5	43.4	152	2 JC7134	agkiscutacin alph
5	296	42.3	144	2 FC7027	aggrelin alpha cha
6	260.5	37.3	146	2 JC7135	agkiscutacin beta
7	254.5	36.4	131	2 JC5058	bitiscetin alpha c
8	237.5	34.0	146	2 JC7105	aggrelin beta chal
9	230.5	33.0	123	2 B42972	coagulation factor
10	208.5	29.8	125	2 JC5059	bitiscetin beta ch
11	204.5	29.3	146	2 JC4691	coagulation factor
12	203.5	29.1	125	2 B47267	botrocetin beta ch
13	191.5	27.4	123	2 JC2415	echlocetin beta cha
14	181	25.9	166	2 RGH01A	regenerating islet
15	181	25.9	166	2 A45751	pancreatic stone p
16	176.5	25.3	175	2 S29822	pancreatitis-assoc
17	176	25.2	40	2 S56006	pancreatic stone p
18	169.5	24.2	175	2 A41719	tokaracetin alpha
19	168	24.0	165	2 A47148	reg I, regeneratin
20	167.5	23.0	175	2 A37194	pancreatic thread
21	167	22.9	173	2 B47134	reg II, regenerati
22	166.5	22.8	175	2 A49616	pancreatitis-assoc
23	160	22.9	165	2 A28351	pancreatic stone p
24	160	22.9	166	1 RGHU1B	regenerating islet
25	158	22.6	162	1 LNR01	lectin BRA3-1 prec
26	157	22.5	162	1 LNR03	lectin BRA3-2 prec
27	156	22.0	40	2 S56007	tokaracetin beta c
28	154	22.0	2415	1 A39086	aggrecan precursor
29	153	21.9	174	2 S54979	pancreatitis-assoc

30	151	21.6	2124	2 A28452	proteoglycan core
31	151	21.6	2132	1 A55182	aggrecan precursor
32	147.5	21.1	912	2 A54423	brevican precursor
33	147	21.0	40	2 B56829	alboaggrelin-B alp
34	146.5	21.0	883	2 S57653	brevican precursor
35	146.5	21.0	1463	2 A53210	phospholipase A2 r
36	146	20.9	1340	2 A39808	proteoglycan core
37	146	20.9	2327	2 T42630	aggrecan - bovine
38	145.5	20.8	330	2 T46256	brevican - human (
39	145	20.7	1487	2 S48719	phospholipase-A(2)
40	144.5	20.7	883	2 S49126	brevican precursor
41	143	20.5	135	2 A38609	lectin, galactose-
42	140	20.0	2109	1 T50421	aggrecan precursor
43	139.5	20.0	178	2 T29536	hypothetical prote
44	139	19.9	1268	2 S52781	neurocan - mouse
45	138	19.7	1257	2 S28764	neurocan precursor

#### ALIGNMENTS

##### RESULT 1

JC4329 coagulation factor IX-binding protein A chain - habu

C:Species: Trimeresurus flavoviridis (habu)

C>Date: 06-Dec-1995 #sequence\_revision 08-Feb-1996 #text\_change 13-Mar-1998

C:Accession: JC4329

R:Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.

J. Biochem. 118, 965-973, 1995

A:Title: Blood coagulation factor IX-binding protein from the venom of Trimeresurus f

A:Reference number: JC4329; MUID:96318509

A:Accession: JC4329

A:Molecule type: protein

A:Residues: 1-129 <ATO>

C:Comment: This protein binds calcium.

C:Superfamily: tetraacetin; C-type lectin homology

C:Keywords: anticoagulant; blood coagulation; calcium binding; venom

F:2-127/Domain: C-type lectin homology <LCH>

F:2-13,30-127,102-119/Disulfide bonds: #status predicted

Query Match 49.3%; Score 344.5; DB 2; Length 129;  
Best Local Similarity 48.4%; Pred. No. 1.7e-28;  
Matches 62; Conservative 24; Mismatches 33; Indels 9; Gaps 2;

OY 3 ECPGSMSSYDRYCKYKPKFQEMTWADQRCSEQAKGHLISVETALASFYDNVLYANKE 62

DB 1 DCPGSMSSYEGHCYKPKFLKXTWDAERFCTPQAKGHVTSAGADPVAQLVTENIQ 60

OY 63 YLTIRIWIIGLRVQNGQPC-----SSISTYBNLYDPPE--CFMVSQDTRLEMEKRVDC 113

DB 61 NTKSYWVWIGLRQGEKQCSSEMSDSSVSSEWNIIEASKTCLGKETGFRKWNIVYG 120

OY 114 QOHSFICK 121

DB 121 QQNPVCE 128

##### RESULT 2

A47267 botrocetin alpha chain - jararaca

N:Alternate names: two chain botrocetin alpha chain

C:Species: Bothrops jararaca (jararaca)

C>Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-May-1998

C:Accession: A47267; B37958

R:Usami, Y.; Fujimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.

Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993

A:Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator

A:Reference number: A47267; MUID:93157385

A:Accession: A47267

A:Molecule type: protein

A:Residues: 1-133 <USA>

A:Experimental source: venom



```

OY      3  ECEBGESSYRUCYKCFKPEKCOMETADQRCSPQAKGHLLSVETLASEFVDNYLYAKE 62
      :  ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db      12 DCDGMSRPYDHCYQAFNEBKTWDEAKFCKRQENGAHLLASTIENSGADFW-SWLSQKD 70

OY      63 YLR--RTWIGLGVNKKGPC-----SSISEYNYLD--PPECFMVSBDRLREMEKVD 111
      :  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      71 ELADEDEYVWIGLQAKNEQDCSSMSDGSVSSTENLLDLTKKCGALEKLVGFRKMYNY 130

OY      112 GEQHSFICK 121
      ||| ||| : |||
Db      131 GEQMHAFVCK 140

```

RESULT 6  
JC7135  
agkissactacin beta chain precursor - sharp-nosed viper  
N:Alternate names: fibrinogenlytic venom protein  
C:Species: Agkistrodon acutus (Sharp-nosed viper)  
C:Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 24-Oct-2000  
C:Accession: JC7135; PC7038  
R:Chem. X.: Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu J.  
Biochem. Biophys. Res. Commun. 265, 530-535, 1999  
A:Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic venom  
A:Reference number: JC7134; M0ID:20025379  
A:Accession: JC7135  
A:Molecule type: mRNA  
A:Residues: 1-146 <CHE>  
A:Cross-references: GB:AF176421  
A:Experimental source: venom gland  
A:Accession: PC7038  
A:Molecule type: protein  
A:Residues: 24-50;59-83;102-107;112-114 <CH2>  
C:Superfamily: tetranectin; C-type lectin homology  
C:Keywords: disulfide bond; heterodimer; venom  
F:1-23/Domains: signal sequence #status predicted <SIG>  
F:24-146/Product: agkissactacin beta chain #status experimental <MAT>

[illegible]

RESULT 7

JC5058

bitiscetin alpha chain - puff adder

N:Alternate names: von Willebrand factor modulator protein

C:Species: Bitis arietans (puff adder)

C:Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 12-Feb-1999

C:Accession: JC5058; JC5916

R:Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Ozaki, Y. Submitted to JIPID, January 1997

A:Description: Complete amino acid sequence of bitiscetin, a novel von willebrand factor

A:Reference number: JC5058

A:Contents: snake venom

A:Accession: JC5058

A:Molecule type: protein

A:Residues: 1-131 <MAT>

A:Experimental source: snake venom

R:Matsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Ozaki, Y. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997

A:Title: Complete amino acid sequence of bilirubin, a novel von Willebrand factor modulator  
A:Reference number: JCS5916  
A:Accession: JCS5916  
A:Molecule type: protein  
A:Residues: 1-131 <MA2>  
A:Experimental source: venom  
A:Comment: This protein is a modulator of a von Willebrand factor modulator.  
C:Superfamily: tetranectin; C-type lectin homology  
C:Keywords: venom  
F:4-125/Domain: C-type lectin homology <LCH>

```

Query Match          36.4% Score 254.5 DB 2 Length 131,
Best Local Similarity 39.3%, Pred. No. 3.6e19,
Matches 53; Conservative 24; Mismatches 43; Indels 15; Gaps 4;

QY 1 DLEPCSGMSYRYRYCYKFKCFKQEMTWADAQRFCSQKAGSHLSTVEATLSEAFVDNVLN 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DPQCILPDMSSYGHGHCYKFKKYGVTWEDAKFEVENS--GHLASIDSKREADVYTKLA--- 55

QY 61 KEYLTRYI--WIGLRVONKGPQPC-----SSISEYENLVDFECPMWSRDTLRWEMEKV 110
    | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db 56 SQTLLKFEYVDADIGLRDESKTQCQCSPPQMTDGSVYAYENVDDEPTKCGFLDHTREYRTWDL 115

QY 111 DCEQGHSTFICKTRP 125
    | : : : | | | | | |
Db 116 PCGEKNPFICKSRLP 130

```

```

RESULT      8
JC7105
aggreitin beta chain - Malayan pit viper
C:Species: Calloselasma rhodostoma (Malayan pit viper)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C:Accession: JC7105
R:Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A:Title: Molecular cloning and sequence analysis of aggreitin, a collagen-like platelet
A:Reference number: PC7027; MUID:99443731
A:Accession: JC7105
A:Molecule type: mRNA
A:Residues: 1-146 <CHU>
A:Experimental source: venom gland
C:Superfamily: tetraneurin; C-type lectin homology
C:Keywords: disulfide bond; platelet aggregation; venom

```

Query Match	Similarity	34.0%;	Score 237.5;	DB 2;	Length 146;
Best Local	Similarity	38.6%;	Pred. No. 2.4e-17;		
Matches	Conservative	19;	Mismatches	46;	Indels 13; Gaps 5
QY	3	ECPCGMSYDRCYCPFKQEMTWADQRCFSQAKGHLISVETALAEAFVNVLYANKE	62		
	:		:		
DB	24	DQPCGMSSTEGHCKYRFPNEPKMWADERCKIQPKHSHLSVQSALAEAFV--VKLTRR	81		
QY	63	YLTRITGLRYGNCQGPC-----SSISYENLYDPFEFCFVSRDTRLREMFKYDCEQ	115		
	:		:		
DB	82	LKANLYMWGL--SNIVHGNCNQWQSDGARLNYKDWQSQSBC-LAFRGVH-TWILNMDCSST	137		
QY	116	HSFICKF	122		
	:		:		
DB	138	CSFVCKF	144		

RESULT 9  
BA2972  
coagulation factor X activating enzyme (EC 3.4.24. ) light chain - Russell's viper  
C.Species: *Vipera russelli* (Russell's viper)  
C.Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Feb-1997  
C.Accession: BA2972  
R.Takaya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Salsaka, Y.; Morita, T.; Iwanaga, T. Biol. Chem. 267, 14109-14117, 1992  
A.Title: Coagulation factor X activating enzyme from Russell's viper venom (RVV-X). A



A:Note: sequence extracted from NCBI backbone (NCBI:P124086)  
 R:Fujimura, Y.; Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug  
 Biochemistry 30, 1957-1964, 1991  
 A:Title: Isolation and chemical characterization of two structurally and functionally di  
 A:Reference number: A37958; MUID:91129280  
 A:Accession: C37958  
 A:Molecule type: protein  
 A:Residues: 1-40 <FUJ>  
 C:Complex: heterodimer of alpha (see PIR:A47267) and beta chains  
 C:Superfamily: tetralectin; C-type lectin homology  
 C:Keywords: hemagglutinin; heterodimer; venom  
 F:2-121/Domain: C-type lectin homology <LCH>  
 F:2-13,30-112,98-113/Disulfide bonds: #status experimental  
 F:75/Disulfide bonds: interchain (to alpha-80) #status experimental

Query Match 29.1%; Score 203.5; DB 2; Length 125;  
 Best Local Similarity 35.9%; Pred. No. 6.7e-14;  
 Matches 47; Conservative 26; Mismatches 39; Indels 19; Gaps 8;

OY 3 ECPSGMSYRCYCKPKPKQMTADAFQCEQAKGGHLSVETALSFVNDVLYANKE 62  
 DB 1 DCPDPMSSYCHCTKRFKEMHMDAEFCBQGTGAHLVSFQSKKEADFYRSL---TSE 57  
 OY 63 YLR-RYIMIGLR-VONKGPC-----SSISYEN-LVDPFECFMYSRDRLREMFYVD 111  
 DB 58 MLKGDYVWIGLSDPVWKN---CRFEWTDGMEDPDYDYLIAIEYC-VASKPIN-NKMWIIP 112  
 OY 112 CEQOHSPTCKF 122  
 DB 113 CTRFKNFVCEP 123

RESULT 13  
 JC2415  
 echicetin beta chain - saw-scaled viper  
 C:Species: Echis carinatus (saw-scaled viper)  
 C:Date: 21-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 15-Oct-1996  
 C:Accession: JC2415  
 R:Peng, M.; Holt, J.C.; Niewiarowski, S.  
 Biochem. Biophys. Res. Commun. 205, 68-72, 1994  
 A:Title: Isolation, characterization and amino acid sequence of echicetin beta subunit,  
 A:Reference number: JC2415; MUID:95091801  
 A:Accession: JC2415  
 A:Molecule type: protein  
 A:Residues: 1-123 <PEN>  
 A:Experimental source: venom  
 C:Comment: This protein inhibits agglutination of fixed platelets induced by several pla  
 11edrand factor and albosagregins.  
 C:Superfamily: tetralectin; C-type lectin homology  
 C:Keywords: anticoagulant; dimer  
 F:2-119/Domain: C-type lectin homology <LCH>  
 F:2-13,30-119,96-111/Disulfide bonds: #status predicted

Query Match 27.4%; Score 191.5; DB 2; Length 123;  
 Best Local Similarity 31.2%; Pred. No. 1.2e-12;  
 Matches 39; Conservative 24; Mismatches 49; Indels 13; Gaps 4;

OY 4 CPSPGMSYDYRCYKPKPKQMTADAFQCEQAKGGHLSVETALSFVNDVLYANKE 63  
 DB 2 CLPDMSSYCHCTKRFKEMHMDAEFCBQGTGAHLVSFQSKKEADFYRSL---TSE 57  
 OY 64 LRRYIMIGLR-VONKGPC-----SSISYEN-LVDPFECFMYSRDRLREMFYVD 116  
 DB 61 -MLVWIGL--SDYWRRCYEWMSDGAQLDYKAWDNERHCF--AAKTTDNCMMRRKCGSEF 115  
 OY 117 SPFCK 121  
 DB 116 YFVCK 120

RESULT 14

RGHUA  
 regenerating islet lectin 1-alpha precursor [validated] - human  
 M:Alternate names: lithostathine; pancreatic thread protein (PTP); reg I protein; reg  
 N:Contains: pancreatic stone protein (PSP)  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1990 #sequence\_revision 03-Aug-1995 #text\_change 08-Dec-2000  
 C:Accession: A35197; B28351; S12950; S02767; S02419; S00113; S01471; A25246  
 R:Watanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.  
 J. Biol. Chem. 265, 7432-7439, 1990  
 A:Title: Complete nucleotide sequence of human reg gene and its expression in normal  
 product of the gene.  
 A:Reference number: A35197; MUID:90237042  
 A:Accession: A35197  
 A:Molecule type: DNA  
 A:Residues: 1-166 <WAT>  
 A:Cross-references: GB:J05412  
 R:Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; Yonemura, Y.; Tochino, Y.; Oka  
 J. Biol. Chem. 263, 2111-2114, 1988  
 A:Title: A novel gene activated in regenerating islets.  
 A:Reference number: A92704; MUID:88115343  
 A:Accession: B28351  
 A:Molecule type: mRNA  
 A:Residues: 1-166 <TER>  
 A:Cross-references: GB:M8963; NID:9190978; PID:AAA36558.1; PID:9190979  
 R:Itch, T.; Tsuzuki, H.; Kato, T.; Teraoka, H.; Matsumoto, K.; Yoshida, N.; Terazono  
 FEBS Lett. 272, 85-88, 1990  
 A:Title: Isolation and characterization of human reg protein produced in Saccharomyce  
 A:Reference number: S12950; MUID:91032149  
 A:Accession: S12950  
 A:Molecule type: protein  
 A:Residues: 23-52;160-166 <ITC>  
 A:Note: sequence determined from protein isolated after human cDNA sequence was clone  
 R:de Caro, A.M.; Adrich, Z.; Pournet, B.; Capon, C.; Bonicel, J.J.; de Caro, J.D.; Ro  
 Biochim. Biophys. Acta 994, 281-284, 1989  
 A:Title: N-terminal sequence extension in the glycosylated forms of human pancreatit  
 A:Reference number: S02767; MUID:89150292  
 A:Accession: S02767  
 A:Molecule type: protein  
 A:Residues: 23-47 <DEC>  
 R:Bonimi, P.; de Caro, J.; Bonicel, J.; Rovey, M.; de Caro, A.  
 FEBS Lett. 229, 171-174, 1988  
 A:Title: The disulfide bridges of the immunoreactive forms of human pancreatic stone  
 A:Reference number: S02419; MUID:88152214  
 A:Accession: S02419  
 A:Molecule type: protein  
 A:Residues: 63-72;125-139;150-157;160-166 <ROU>  
 A:Note: disulfide bonds  
 R:de Caro, A.M.; Bonicel, J.J.; Rouimi, P.; de Caro, J.D.; Sarles, H.; Rovey, M.  
 Eur. J. Biochem. 168, 201-207, 1987  
 A:Title: Complete amino acid sequence of an immunoreactive form of human pancreatic s  
 A:Reference number: S00113; MUID:88029417  
 A:Accession: S00113  
 A:Molecule type: protein  
 A:Residues: 34-166 <DEL>  
 R:Rouimi, P.; Bonicel, J.; Rovey, M.; de Caro, A.  
 FEBS Lett. 216, 195-199, 1987  
 A:Title: Cleavage of the Arg-116 bond in the native polypeptide chain of human pancre  
 A:Reference number: S01471; MUID:87219142  
 A:Accession: S01471  
 A:Molecule type: protein  
 A:Residues: 33-48 <ROZ>  
 R:Montalto, G.; Bonicel, J.; Multigner, L.; Rovey, M.; Sarles, H.; De Caro, A.  
 Biochem. J. 238, 227-232, 1986  
 A:Title: Partial amino acid sequence of human pancreatic stone protein, a novel pancr  
 A:Reference number: A25246; MUID:87099950  
 A:Accession: A25246  
 A:Molecule type: protein  
 A:Residues: 34-73,'X',75-87,'R',89-98 <MON>  
 C:Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like c  
 C:Genetics: Intact regenerating islet lectin 1-alpha, lithostathine, inhibits the grow  
 A:Gene: GDB:REG  
 A:Cross-references: GDB:132455; OMIM:167770



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 3, 2002, 16:25:11 ; Search time 11.83 Seconds  
(without alignments)  
412.398 Million cell updates/sec

Title: US-09-926-256-1  
Perfect score: 699  
Sequence: 1 DLECPGWSYDRYCYRPFK.....WFKYDCEQHSFICKTRPR 126

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349.5	50.0	133	1	RHCA_AGRH
2	338.5	48.4	131	1	ABAI_TRIAB
3	323	46.2	133	1	BOTR_BOTJA
4	322.5	46.1	132	1	ABBA_TRIAB
5	318.5	45.6	134	1	ABAA_TRIAB
6	316.5	45.3	129	1	RHCB_AGRH
7	314.5	45.0	152	1	IXA_TRIFL
8	264.5	37.8	123	1	ABAA_TRIAB
9	264.5	37.8	133	1	ECNA_ECHCA
10	203.5	29.4	125	1	ABAA_TRIAB
11	204.5	29.3	146	1	IXB_TRIFL
12	203.5	29.1	125	1	BOTR_BOTJA
13	191.5	27.4	123	1	ECNB_ECHCA
14	187.5	26.8	118	1	ABBA_TRIAB
15	181	25.9	166	1	LITH_HUMAN
16	176.5	25.3	175	1	PAP1_MOUSE
17	169.5	24.2	175	1	PAP1_RAT
18	168	24.0	165	1	LITH_MOUSE
19	167.5	24.0	175	1	LITH_BOVIN
20	167	23.9	173	1	LITH_MOUSE
21	166.5	23.8	175	1	PAP1_HUMAN
22	160	22.9	165	1	LITH_RAT
23	160	22.9	166	1	LITH_HUMAN
24	157	22.5	162	1	LECG_MEGRO
25	154	22.0	2415	1	PGCA_MEGRO
26	153	21.9	174	1	PAP3_RAT
27	151	21.6	2124	1	PGCA_RAT
28	151	21.6	2132	1	PGCA_MOUSE
29	150	21.5	174	1	PAP3_MOUSE
30	147.5	21.1	912	1	PGCB_BOVIN
31	146.5	21.0	175	1	PGCB_HUMAN
32	146.5	21.0	883	1	PGCB_MOUSE
33	146.5	21.0	1463	1	PAP2_BOVIN

34	146	20.9	2364	1	PGCA_BOVIN
35	144.5	20.7	883	1	PGCB_RAT
36	143	20.5	135	1	LECG_CROAT
37	140	20.0	2109	1	PGCA_CHICK
38	139	19.9	1268	1	PGCN_MOUSE
39	138	19.7	1257	1	PGCN_RAT
40	134	19.2	147	1	LECG_ANTCR
41	134	19.2	2333	1	PGCA_CANFA
42	133.5	19.1	1458	1	PAP2_RABIT
43	132.5	19.0	172	1	LECG_PLEMA
44	132.5	19.0	175	1	PAP2_MOUSE
45	131	18.7	122	1	LITH_PIG

## ALIGNMENTS

```

RESULT 1
RHCA_AGRH STANDARD: PRT; 133 AA.
ID P81397;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Rhodocetin alpha subunit.
OS Agkistrodon rhodostoma (Malayan pit viper) (Crotalidae: Serpentes; Colubroidae).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scieroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Callisela.
OX NCBI_TaxID=8717;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Wang R, Kini M, Chung M.C.M.;
RL Submitted (JUN-1998) to the SWISS-PROT data bank.
CC -I- SUBUNIT: HETERODIMER OF TWO ALPHA SUBUNITS AND ONE BETA SUBUNIT.
CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN DOMAIN.
DR HSSP; P23806; IIXX.
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c.1.
DR SMART; SMO0034; CLECT.1.
DR PROSITE; PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
KW Venom; Lectin.
FT DOMAIN 1 129 C-TYPE LECTIN (LONG FORM).
FT DISULFD 2 13 BY SIMILARITY.
FT DISULFD 30 127 BY SIMILARITY.
FT DISULFD 102 119 BY SIMILARITY.
SQ SEQUENCE 133 AA; 15962 MW; 386EAC519DFC674D CRC64;

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Query Match 50.0%; Score 349.5; DB 1; Length 133;  
Best Local Similarity 48.1%; Pred. No. 4,6e-30;  
Matches 64; Conservative 24; Mismatches 36; Indels 9; Gaps 2;

```

QY 3 ECPGWSYDRYCYRPFKQEMTADQRCFSQANGHLISVETALASVDNYANKE 62
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DCPDMSSTKSYCRPFKEKTEBERCTQEKRAHLVSMENRLEAVFVDMYENNE 60
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 63 YLIRYIWGLRQNGQRC-----SSTSYENLVDPF--ECFMSRQRLKEWFEVDE 113
   ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 NKIYRWGLKLENGQSRNLEMSDSSISYENLYEYKCFMDHQSLPRWHTADE 120
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 114 QHNSFICKTRPR 126
   :||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 EKNVWCKFOLPR 133

```

RESULT 2  
ABAI\_TRIAB STANDARD: PRT; 131 AA.  
ID P8111;  
DT 15-JUL-1998 (Rel. 36, Created)

```
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
OS Alboggregin A subunit 1.
DE Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperoidea; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
RA Calvete J.J., Niewiarowski S.;
RT "Alboggregins A and B. Structure and interaction with human
RT platelets."
RL Thromb. Haemost. 79:609-613(1998).
CC -1- FUNCTION: BINDS TO PLATELET GPIIb/IIIa RECEPTOR SYSTEM AND STIMULATES
CC AGGUTINATION.
CC -1- SUBUNIT: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4,
CC DISULFIDE-LINKED.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
CC HSSP: P23806; IIX.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KM Venom; Lectin. 1 129 C-TYPE LECTIN (LONG FORM).
FT DOMAIN 2 13 BY SIMILARITY.
FT DISULFID 30 127 BY SIMILARITY.
FT DISULFID 102 119 BY SIMILARITY.
FT DISULFID 131 AA; 15427 MW; B3569F5BP91F6624 CRC64;
SQ SEQUENCE

Query Match 48.4%; Score 338.5; DB 1; Length 131;
Best Local Similarity 47.3%; Pred. NO. 6.5e-29;
Matches 62; Conservative 21; Mismatches 39; Indels 9; Gaps 2;

OY 3 ECPSSMSYGRYCKPKPKQEMTWADQRFCSQAKGHLISYETALASFDVNLVANK 62
DB 1 DCPSSMSYDGYCYKRVKRIQTIWEDAEKRFCSQANDGHLVIESAGEAFVQLVSENIR 60
OY 63 YLTRYIWIIGLRVQKKGOPC-----SSISYENLVDP--PFCFNVSRDTRLREMFVDC 113
DB 61 SEKHYYWIGLRVQKKGQCCSEMSDGSVHVNDLGNKTRKCYGLEKRAEPRFVWNVYCG 120
OY 114 QQHSFICKFTR 124
DB 121 HEYFVCKEYR 131

RESULT 3
BOTA_BOTJA STANDARD; PRT: 133 AA.
ID BOTA_BOTJA
AC P22029;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Botrocetin, alpha chain (Platelet coagglutinin).
OC Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperoidea; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RA MEDLINE=93157385; PubMed=8430107;
RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
RA Titani K.;
RT "Primary structure of two-chain botrocetin, a von Willebrand factor
```

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RT modulator purified from the venom of Bothrops jararaca.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
RN
RP SEQUENCE OF 1-40.
RC TISSUE=Venom;
RA MEDLINE=91129280; PubMed=1993206;
RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,
RA Fukui H., Sugimoto M., Ruggieri Z.M.;
RT "Isolation and chemical characterization of two structurally and
RT functionally distinct forms of Bothrops jararaca.";
RL Biochemistry 30:11957-11964(1991).
CC -1- FUNCTION: TWO-CHAIN BOTROCETIN FORMS AN ACTIVATED COMPLEX WITH
CC VWF, AND THE COMPLEX THEN BINDS TO PLATELET GPIIb, RESULTING IN
CC PLATELET AGGUTINATION.
CC -1- FUNCTION: THERE ARE TWO DISTINCT FORMS OF THE VON WILLEBRAND
CC FACTOR-DEPENDENT PLATELET COAGGLUTININ. THE DIMERIC FORM IS
CC 34-TIMES MORE ACTIVE THAN THE ONE-CHAIN BOTROCETIN IN PROMOTING
CC VWF BINDING TO PLATELETS.
CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF AN ALPHA AND A BETA CHAIN.
CC VWF AND BOTROCETIN FORM A SOLUBLE COMPLEX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.
CC PIR: B37958; B37958.
DR PIR: A47267; A47267.
DR HSSP: P23806; IIX.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KM Venom; Lectin. 2 13
FT DISULFID 30 128 INTERCHAIN (WITH C-75 IN BETA CHAIN).
FT DISULFID 80 80
FT DISULFID 103 120
SQ SEQUENCE 133 AA; 15215 MW; E4CF4502946AC74B CRC64;

Query Match 46.2%; Score 323; DB 1; Length 133;
Best Local Similarity 46.6%; Pred. No. 2.9e-27;
Matches 62; Conservative 25; Mismatches 36; Indels 10; Gaps 3;

OY 3 ECPSSMSYDRYCYKPFQKQEMTWADQRFCSQAKGHLISYET-ALASFDVNLVANK 61
DB 1 DCPSSMSYEGYCYKPFQKQMWADAERKCSQAKGHLISYIKYKQFVDDLVKNI 60
OY 62 YLTRYIWIIGLRVQKKGOPC-----SSISYENLVDPF--ECFNVSRDTRLREMFVDC 112
DB 61 QSSDIYAMIGLRVENKKEKCCSEMSDGSYSYENYERYVKKCFALKDLGFLVIMNLVC 120
OY 113 EQQHSFICKFTRP 125
DB 121 AQKNFVCKSP 133

RESULT 4
ABBA_TRIAB STANDARD; PRT: 132 AA.
ID ABBA_TRIAB
AC P81115;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Alboggregin B alpha subunit.
OC Trimeresurus albolabris (White-lipped pit viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperoidea; Crotalinae; Trimeresurus.
OX NCBI_TaxID=8765;
RN
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=98189535; PubMed=9531050;
RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
```







OY 112 CEOHSHFICKF 122  
 DB 111 CSSTHSFVCE 121

RESULT 9  
 ECHA\_ECHCA STANDARD; PRT; 133 AA.

AC P81017;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Echicetin alpha subunit.  
 OS Echis carinatus (Saw-scaled viper).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Echis.  
 NCBI\_TaxID=40353;

RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=97250657; PubMed=9163349;  
 RA Polgar J., Magneat E.M., Peltsch M.C., Wells T.N.C., Saqi M.S.A.,  
 RA Clemetson K.J.;  
 RT "Amino acid sequence of the alpha subunit and computer modelling of  
 RT the alpha and beta subunits of echicetin from the venom of Echis  
 RT carinatus (saw-scaled viper).";  
 RL Biochem. J. 323:533-537(1997).  
 RN [2]

RC CHARACTERIZATION.  
 RX MEDLINE=93244424; PubMed=8481512;  
 RA Peng M., Lu W., Bevilgia L., Niewiarowski S., Kirby E.P.;  
 RT "Echicetin: a snake venom protein that inhibits binding of von  
 RT Willebrand factor and alphaaggregins to platelet glycoprotein IIb";  
 RL Blood 81:2321-2328(1993).  
 CC -1- FUNCTION: BINDS TO PLATELET GPIIb AND INHIBITS PLATELET  
 CC AGGUTINATION.  
 CC -1- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 DR HSSP: P23806; IIXX.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF000059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C-TYPE LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C-TYPE LECTIN\_2; 1.

KW Venom; Lectin.  
 FT DISULFID 4 15 BY SIMILARITY.  
 FT DISULFID 31 127 BY SIMILARITY.  
 FT DISULFID 102 119 BY SIMILARITY.  
 FT DISULFID 81 81 INTERCHAIN (WITH C-75 IN BETA CHAIN) (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 133 AA; 15803 MW; 8F11C2DBDC70B16 CRC64;

Query Match 37.8%; Score 264.5; DB 1; Length 133;  
 Best Local Similarity 37.8%; Pred. NO. 4.3e-21;  
 Matches 51; Conservative 32; Mismatches 41; Indels 11; Gaps 4;

OY 1 DLPCPSGMSYDRCYCPFKOEMTWADAPRCSEQAKGHLISYETALEASFVNVLKAN 60  
 DB 1 DQDLSGMSYEGGHCYDFLRK-TWDEAKYCN-QMDGHLVSTSNKAKAEFVAQLIRK 58  
 OY 61 --KEYLRITWIGLRVONKQGPC-----SSISYENLVDFECFVNSRDTLRLEWFKVD 111  
 DB 59 LPKSAIDRWVIGLRDRSKRCQGLWLTNDSFVYEHVVPPTKCFVLEQRQTEFRKVIAYN 118  
 OY 112 CEOHSHFICKFTRR 126  
 DB 119 CEKFPFVCAKIPR 133

RESULT 10  
 ABA3\_TRIAB STANDARD; PRT; 125 AA.

AC P81113;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Alboaggregin A subunit 3.  
 OS Trimeresurus albolabris (White-lipped pit viper).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Chordata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 NCBI\_TaxID=8765;

RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=98189535; PubMed=9531050;  
 RA Kowaleka M.A., Tan L., Holt J.C., Peng M., Karczewski J.,  
 RA Calvete J.J., Niewiarowski S.;  
 RT "Alboaggregins A and B. Structure and interaction with human  
 RT platelets";  
 RL Thromb. Haemost. 79:609-613(1998).  
 CC -1- SUBUNIT: BINDS TO PLATELET GPIIb/IX RECEPTOR SYSTEM AND STIMULATES  
 CC AGGUTINATION.  
 CC -1- FUNCTION: HETEROTETRAMER OF THE SUBUNITS 1, 2, 3 AND 4,  
 CC DISULFIDE-LINKED.  
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.  
 DR HSSP: P23807; IIXX.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF000059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C-TYPE LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C-TYPE LECTIN\_2; 1.

KW Venom; Lectin.  
 FT DOMAIN 3 123 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 4 15 BY SIMILARITY.  
 FT DISULFID 32 121 BY SIMILARITY.  
 FT DISULFID 98 113 BY SIMILARITY.  
 SQ SEQUENCE 125 AA; 14798 MW; CAFE24C098DF3293 CRC64;

Query Match 29.4%; Score 205.5; DB 1; Length 125;  
 Best Local Similarity 33.9%; Pred. NO. 6.7e-15;  
 Matches 43; Conservative 24; Mismatches 47; Indels 13; Gaps 5;

OY 3 ECPSPGMSYDRCYCPFKOEMTWADAPRCSEQAKGHLISYETALEASFVNVLKANKE 62  
 DB 3 DCPFGMSYEGCYVYKKNKMMWDAESFCROHRSKSHVSHSGEVDVFSKFFPILR 62  
 OY 63 YLTRITWIGLRVONKQGPCSS-----ISYENLVDFECFVNSRDTLRLEWFKYDCQO 115  
 DB 63 Y-DEVWMLG-SDIWKECTKEMSDGARLDYKAWSGSKSYC-LVSKYTN-NEWLSMDCSRT 116  
 OY 116 HSFICKF 122  
 DB 117 RYPVCKF 123

RESULT 11  
 IXB\_TRIFL STANDARD; PRT; 146 AA.

AC P23807; Q91247;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Coagulation factor IX/factor X-binding protein B chain precursor  
 DE (IX/X-BP).  
 OS Trimeresurus flavoviridis (Habu).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Chordata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 NCBI\_TaxID=88087;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=96184662; PubMed=8645314;  
 RA Matsuzaki R., Yoshihara E., Yamada M., Shima K., Atoda H., Morita T.;  
 RT "CDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant  
 RT protein from snake venom.";  
 RL Biochem. Biophys. Res. Commun. 220:382-387(1996).  
 RN [2]  
 RP SEQUENCE OF 24-146.  
 RC TISSUE=Venom;  
 RX MEDLINE=91352000; PubMed=1831197;  
 RA Atoda H., Hyuga M., Morita T.;  
 RT "The primary structure of coagulation factor IX/factor X-binding  
 RT protein isolated from the venom of *Trimeresurus flavoviridis*.  
 RT Homology with asialoglycoprotein receptors, proteoglycan core  
 RT protein, tetraectin, and lymphocyte Fc epsilon receptor for  
 RT immunoglobulin E.";  
 RL J. Biol. Chem. 266:14903-14911(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=97331317; PubMed=9187649;  
 RA Mizuno H., Fujimoto Z., Kozumi M., Kano H., Atoda H., Morita T.;  
 RT "Structure of coagulation factors IX/X-binding protein, a heterodimer  
 RT of C-type lectin domains.";  
 RL Nat. Struct. Biol. 4:438-441(1997).  
 CC -1- FUNCTION: ANTICOAGULANT PROTEIN WHICH BINDS WITH FACTOR IX AND  
 CC FACTOR X IN THE PRESENCE OF CALCIUM WITH A 1 TO 1 STOICHIOMETRY.  
 CC -1- SUBUNIT: HETERODIMER OF CHAINS A AND B LINKED BY A DISULFIDE BOND.  
 CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.  
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: D83332; BAA11888.1; .  
 CC PIR: B39332; B39332.  
 CC PDB: 1IXX; 06-MAY-98.  
 CC InterPro: IPR001304; lectin\_c.  
 CC DR Pfam: PF00059; lectin\_c; 1.  
 CC DR SMART: SM00034; CLECT; 1.  
 CC DR PROSITE: PS00615; C\_TYPE\_LECTIN\_1; 1.  
 CC DR PROSITE: PS50041; C\_TYPE\_LECTIN\_2; 1.  
 CC DR Lectin; Calcium; Signal; 3D-structure.  
 CC FT SIGNAL 1 23  
 CC FT CHAIN 24 146 COAGULATION FACTOR IX/FACTOR X-BINDING  
 CC FT DOMAIN 24 144 PROTEIN B CHAIN.  
 CC FT DISULFID 25 144 C-TYPE LECTIN (LONG FORM).  
 CC FT DISULFID 53 142 BY SIMILARITY.  
 CC FT DISULFID 98 98 INTERCHAIN (WITH C-102 OF A CHAIN).  
 CC FT DISULFID 119 134 BY SIMILARITY.  
 CC FT DISULFID 146 134 BY SIMILARITY.  
 CC SEQUENCE 146 AA; 16922 MM; 8E1961C59F6757C CRC64;

Query Match 29.3%; Score 204.5; DB 1; Length 146;  
 Best Local Similarity 33.9%; Pred. No. 1e-14;  
 Matches 43; Conservative 23; Mismatches 48; Indels 13; Gaps 4;

OY 3 ECPSSGSSYDRYCYKPKFQEMTWADQRCSEDAKGGHLLSVETALASVDVNYLANKE 62  
 DB 24 DCPDMSWSEYEGHCYKPKFSEPRKMWADAENCTOOHAGHLLSVFOSSEAEFV--VKLAFOT 81  
 OY 63 YLTPYTWIGLAVOKKQGPC-----SSISYENLVDPFECFMYSRDRLREWFKVDCEQ 115  
 DB 82 FGHISIFMWGL--SNVWNOCNMOMNAALRYKAAAE--ESYCYFSTKNNKWRACRAM 137  
 OY 116 HSFICKF 122  
 DB 138 ADFVCEF 144

RESULT 12  
 BOTB\_BOTUA STANDARD; PRT; 125 AA.  
 AC P22030;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Botrocelin, beta chain (platelet coagultinln).  
 OS Botrotops jararaca (jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;  
 OC Viperidae; Crotalinae; Bothrops.  
 NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE=Venom;  
 RX MEDLINE=93157385; PubMed=8430107;  
 RA Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,  
 RA Titani K.;  
 RT "Primary structure of two-chain botrocelin, a von Willebrand factor  
 RT modulator purified from the venom of *Bothrops jararaca*.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).  
 RN [2]  
 RP SEQUENCE OF 1-40.  
 RC TISSUE=Venom;  
 RX MEDLINE=91129280; PubMed=1993206;  
 RA Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T.,  
 RA Fukui H., Sugimoto M., Ruggeri Z.M.;  
 RT "Isolation and chemical characterization of two structurally and  
 RT functionally distinct forms of botrocelin, the platelet coagultinln  
 RT isolated from the venom of *Bothrops jararaca*.";  
 RL Biochemistry 30:1957-1964(1991).  
 CC -1- FUNCTION: TWO-CHAIN BOTROCELIN FORMS AN ACTIVATED COMPLEX WITH  
 CC VWF, AND THE COMPLEX THEN BINDS TO PLATELET GPIB, RESULTING IN  
 CC PLATELET AGGUTINATION.  
 CC -1- FUNCTION: THERE ARE TWO DISTINCT FORMS OF THE VON WILLEBRAND  
 CC FACTOR-DEPENDENT PLATELET COAGULOTININ. THE DIMERIC FORM IS  
 CC 34-TIMES MORE ACTIVE THAN THE ONE-CHAIN BOTROCELIN IN PROMOTING  
 CC VWF BINDING TO PLATELETS.  
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF AN ALPHA AND A BETA CHAIN.  
 CC VWF AND BOTROCELIN FORM A SOLUBLE COMPLEX.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC PIR: C37958; C37958.  
 CC PIR: B47267; B47267.  
 CC HSSP: P23807; 1IXX.  
 CC InterPro: IPR001304; lectin\_c.  
 CC DR Pfam: PF00059; lectin\_c; 1.  
 CC DR SMART: SM00034; CLECT; 1.  
 CC DR PROSITE: PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 CC DR PROSITE: PS50041; C\_TYPE\_LECTIN\_2; 1.  
 CC DR Venom; Lectin.  
 CC FT DISULFID 2 13  
 CC FT DISULFID 30 121 INTERCHAIN (WITH C-80 IN ALPHA CHAIN).  
 CC FT DISULFID 75 75  
 CC FT DISULFID 98 113  
 CC SEQUENCE 125 AA; 15037 MM; 1ED2027ED817FCA0 CRC64;

Query Match 29.1%; Score 203.5; DB 1; Length 125;  
 Best Local Similarity 35.9%; Pred. No. 1.1e-14;  
 Matches 47; Conservative 26; Mismatches 39; Indels 19; Gaps 8;

OY 3 ECPSSGSSYDRYCYKPKFQEMTWADQRCSEDAKGGHLLSVETALASVDVNYLANKE 62  
 DB 1 DCPDMSWSEYEGHCYKPKFSEPRKMWADAENCTOOHAGHLLSVFOSSEAEFV--TS 57  
 OY 63 YLT-RTYTWIGLAVOKKQGPC-----SSISYENLVDPFECFMYSRDRLREWFKVD 111  
 DB 58 MKGDPVWVIGLSDVWVK--CRFEMTDGMEFDYDDYLLAEVRC-VASKPTLN-NKMWIIP 112  
 OY 112 CEQHSFICKF 122

Db 113 CTRKNCVCEP 123

## RESULT 13

AC ECHB\_ECHCA STANDARD; PRT; 123 AA.  
 AC P81996;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Echicetin beta subunit.  
 OS Echis carinatus (Saw-scaled viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Echis.  
 NCBI\_TaxID=40353;  
 RX MEDLINE=95091801; PubMed=7999097;  
 RC TISSUE=Venom;  
 RA Peng M., Holt J.C., Niewiarowski S.;  
 RT "Isolation, characterization and amino acid sequence of echicetin beta  
 subunit, a specific inhibitor of von Willebrand factor and thrombin  
 interaction with glycoprotein Ib.";  
 RL Biochem. J. 323:533-537(1997).  
 RN [3]  
 RP SEQUENCE OF 1-30.  
 RC TISSUE=Venom;  
 RX MEDLINE=97250657; PubMed=9163349;  
 RA Polgar J., Magrenat E.M., Peltsch M.C., Wells T.N.C., Saqi M.S.A.,  
 RA Clemetson K.J.;  
 RT "Amino acid sequence of the alpha subunit and computer modelling of  
 the alpha and beta subunits of echicetin from the venom of Echis  
 carinatus (Saw-scaled viper).";  
 RL Biochem. J. 323:533-537(1997).  
 RN [3]  
 RP CHARACTERIZATION.  
 RC TISSUE=Venom;  
 RX MEDLINE=93244424; PubMed=8481512;  
 RA Peng M., Lu W., Bevilacqua L., Niewiarowski S., Kirby E.P.;  
 RT "Echicetin: a snake venom protein that inhibits binding of von  
 Willebrand factor and alpha2aggregrins to platelet glycoprotein Ib.";  
 RL Blood 81:2321-2328(1993).  
 CC -1- FUNCTION: BINDS TO PLATELET GPIIb AND INHIBITS PLATELET  
 AGGUTINATION.  
 CC -1- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 DR HSP: P23807; IIX.  
 DR Interpro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LECTIN\_1; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LECTIN\_2; 1.  
 KW Venom; Lectin.  
 FT DOMAIN 1 121 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 2 13 BY SIMILARITY.  
 FT DISULFID 30 119 BY SIMILARITY.  
 FT DISULFID 75 75 INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (BY  
 SIMILARITY).  
 FT DISULFID 96 111 BY SIMILARITY.  
 SQ SEQUENCE 123 AA: 14869 MW: C42C0AD7CDL18CA6 CRC64;

Query Match 27.4%; Score 191.5; DB 1; Length 123;

Best Local Similarity 31.2%; Pred. No. 2e-13;  
 Matches 39; Conservative 24; Mismatches 49; Indels 13; Gaps 4;

QY 4 CPGSGSSYDRYCKPKPEQMTWADAFRCSEQAKGHLISVETALASFDVNLVYANKY 63  
 DB 2 CLPDMASYEGYCKVFERKNNMADAEKFCMKQYVDGHLVFRNSKEVDFTSLFPAHK- 60  
 QY 64 LTRYIWIGLRVONKQGPC-----SSISYENLVDPFECFVNSRDTRLREWFKVDCEQOH 116

Db 61 -MELWVIGL--SDYWRDCYEWMSDGAQLDYKAMDNERRCF--AAKTTDQNMRRKCSGEF 115

QY 117 SFICK 121

Db 116 YFVCK 120

## RESULT 14

AC ABBT\_TRIAB STANDARD; PRT; 118 AA.  
 AC P81116;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Alboaggregin B beta subunit.  
 OS Trimeresurus albolabris (White-lipped pit viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 NCBI\_TaxID=8765;  
 RX MEDLINE=98189535; PubMed=9531050;  
 RC TISSUE=Venom;  
 RA Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,  
 RA Calvele J.J., Niewiarowski S.;  
 RT "Alboaggregins A and B. Structure and interaction with human  
 platelets.";  
 RL Thromb. Haemost. 79:609-613(1998).  
 CC -1- FUNCTION: BINDS TO PLATELET GPIIb/IX RECEPTOR SYSTEM AND STIMULATES  
 AGGUTINATION.  
 CC -1- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS, DISULFIDE-LINKED.  
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.  
 DR HSP: P23807; IIX.  
 DR Interpro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C\_TYPE\_LECTIN\_2; 1.  
 KW Venom; Lectin.  
 FT DOMAIN 1 118 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 2 13 BY SIMILARITY.  
 FT DISULFID 75 75 INTERCHAIN (WITH C-79 IN ALPHA CHAIN)  
 (BY SIMILARITY).  
 FT DISULFID 96 111 BY SIMILARITY.  
 SQ SEQUENCE 118 AA: 13794 MW: 059EDF6B474C4CE CRC64;

Query Match 26.8%; Score 187.5; DB 1; Length 118;  
 Best Local Similarity 33.3%; Pred. No. 5e-13;  
 Matches 41; Conservative 18; Mismatches 53; Indels 11; Gaps 4;

QY 3 ECPGSGSSYDRYCKPKPEQMTWADAFRCSEQAKGHLISVETALASFDVNLVYANKY 62  
 DB 1 DCPSDMSYDLCYKIVQQRNMWEDAEFCRQHTGSHLSFXXXXXADYFXXXXXXX 60

QY 63 YLTRYI-----WIGLRVQ-NKGQPCSSISYENLVDPFECFVNSRDTRLREWFKVDCEQOH 116

Db 61 XXXXWIGLTDVWACRLQWSDG---TTLSKNMTAESEC--IAKTTDQNMWTRSCSRTY 115

QY 117 SFI 119

Db 116 PFV 118

RESULT 15  
 LITA\_HUMAN STANDARD; PRT; 166 AA.

AC P05451; P11379;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lithostathine I alpha precursor (Pancreatic stone protein) (PSP)  
 DE (Pancreatic thread protein) (PTP) (Islet of Langerhans regenerating  
 DE protein) (REG) (Regenerating protein I alpha) (Islet cells  
 DE regeneration factor) (ICRF).  
 GN REGIA OR REG OR PSPS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=88115343; PubMed=2963000;  
 RA Terazono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y.,  
 RA Tochino Y., Okamoto H.;  
 RT "A novel gene activated in regenerating islets.";  
 RL J. Biol. Chem. 263:2111-2114(1988).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=90237042; PubMed=2332435;  
 RA Matsuda T., Yonekura H., Terazono K., Yamamoto H., Okamoto H.;  
 RT "Complete nucleotide sequence of human reg gene and its expression in  
 RT normal and tumoral tissues. The reg protein, pancreatic stone  
 RT protein, and pancreatic thread protein are one and the same product  
 RT of the gene.";  
 RL J. Biol. Chem. 265:7432-7439(1990).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=89292148; PubMed=2525567;  
 RA Giordani D., Bernard J.-P., Rouquier S., Iovanna J., Sables H.,  
 RA Dagorn J.-C.;  
 RT "Secretory pancreatic stone protein messenger RNA. Nucleotide  
 RT sequence and expression in chronic calcifying pancreatitis.";  
 RL J. Clin. Invest. 84:100-106(1989).  
 RN [4]  
 RN SEQUENCE OF 34-166.  
 RX MEDLINE=88029417; PubMed=3655916;  
 RA de Caro A.M., Bonicel J.J., Rouimi P., de Caro J.D., Sables H.,  
 RA Rovey M.;  
 RT "Complete amino acid sequence of an immunoreactive form of human  
 RT pancreatic stone protein isolated from pancreatic juice.";  
 RL Eur. J. Biochem. 168:201-207(1987).  
 RN [5]  
 RN SEQUENCE OF 34-98.  
 RX MEDLINE=87099950; PubMed=3541906;  
 RA Montalto G., Bonicel J.J., Multigner L., Rovey M., Sables H.,  
 RA de Caro A.M.;  
 RT "Partial amino acid sequence of human pancreatic stone protein, a  
 RT novel pancreatic secretory protein.";  
 RL Biochem. J. 238:227-232(1986).  
 RN [6]  
 RN SEQUENCE OF 34-78.  
 RX MEDLINE=86086356; PubMed=3908481;  
 RA Gross J., Carlson R.I., Brauer A.W., Margolies M.N., Warshaw A.L.,  
 RA Wands J.R.;  
 RT "Isolation, characterization, and distribution of an unusual  
 RT pancreatic human secretory protein.";  
 RL J. Clin. Invest. 76:2115-2125(1985).  
 RN [7]  
 RN SEQUENCE OF 23-47.  
 RX MEDLINE=89150292; PubMed=2493268;  
 RA de Caro A.M., Adrich Z., Fournet B., Capon C., Bonicel J.J.,  
 RA de Caro J.D., Rovey M.;  
 RT "N-terminal sequence extension in the glycosylated forms of human  
 RT pancreatic stone protein. The 5-oxoproline N-terminal chain is O-  
 RT glycosylated on the 5th amino acid residue.";  
 RL Biochim. Biophys. Acta 994:281-284(1989).  
 RN [8]  
 RN SEQUENCE OF 33-58.  
 RX MEDLINE=87219142; PubMed=3108036;  
 RA Rouimi P., Bonicel J.J., Rovey M., de Caro A.;  
 RT "Cleavage of the Arg-Ile bond in the native polypeptide chain of  
 RT human pancreatic stone protein.";  
 RL FEBS Lett. 216:195-199(1987).  
 RN [9]  
 RN IDENTITY OF REG WITH PSP.  
 RX MEDLINE=89350859; PubMed=2764894;  
 RA Stewart T.A.;  
 RT "The human reg gene encodes pancreatic stone protein.";  
 RL Biochem. J. 260:622-623(1989).  
 RN [10]  
 RN DISULFIDE BONDS.  
 RX MEDLINE=91032149; PubMed=2226837;  
 RA Itoh T., Tsuzuki H., Katoh T., Teraoka H., Matsumoto K., Yoshida N.,  
 RA Terazono K., Matsuda T., Yonekura H., Yamamoto H., Okamoto H.;  
 RT "Isolation and characterization of human reg protein produced in  
 RT Saccharomyces cerevisiae.";  
 RL FEBS Lett. 272:85-88(1990).  
 RN [11]  
 RN ALZHEIMER'S DISEASE AND DEVELOPMENTAL EXPRESSION REGULATION.  
 RX MEDLINE=90368981; PubMed=2394826;  
 RA de la Monte S.M., Ozturk M., Wands J.R.;  
 RT "Enhanced expression of an exocrine pancreatic protein in Alzheimer's  
 RT disease and the developing human brain.";  
 RL J. Clin. Invest. 86:1004-1013(1990).  
 RN [12]  
 RN X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
 RX MEDLINE=96256285; PubMed=8654365;  
 RA Bertrand J.A., Pignol D., Bernard J.-P., Verdier J.-M., Dagorn J.-C.,  
 RA Fontecilla-Camps J.C.;  
 RT "Crystal structure of human lithostathine, the pancreatic inhibitor  
 RT of stone formation.";  
 RL EMBO J. 15:2678-2684(1996).  
 RN [13]  
 RN X-RAY CRYSTALLOGRAPHY (1.30 ANGSTROMS) OF 23-166.  
 RX MEDLINE=20092874; PubMed=10625646;  
 RA Gerbaud V., Pignol D., Loret E., Bertrand J.A., Verdier J.M.,  
 RA Fontecilla-Camps J.C., Canseller J.P., Gabas N., Verdier J.M.;  
 RT "Mechanism of calcite crystal growth inhibition by the N-terminal  
 RT undecapeptide of lithostathine.";  
 RL J. Biol. Chem. 273:1057-1064(2000).  
 RN [14]  
 RN STRUCTURE BY NMR OF 34-164.  
 RX MEDLINE=97120677; PubMed=8961348;  
 RA Patard L., Stoven V., Charib B., Bontems F., Lallemand J.-Y.,  
 RA de Reggi M.;  
 RT "What function for human lithostathine? structural investigations by  
 RT three-dimensional structure modeling and high-resolution NMR  
 RT spectroscopy.";  
 RL Protein Eng. 9:949-957(1996).  
 CC -1- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM  
 CC CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL  
 CC SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION.  
 CC -1- TISSUE SPECIFICITY: IN PANCREATIC ACINAR CELLS AND, IN LOWER  
 CC LEVELS, IN BRAIN.  
 CC -1- DEVELOPMENTAL STAGE: HIGH EXPRESSION LEVELS IN FETAL AND INFANT  
 CC BRAINS; MUCH LOWER IN ADULT BRAINS.  
 CC -1- DISEASE: ALZHEIMER'S DISEASE AND DOWN'S SYNDROME PATIENTS SHOW  
 CC ENHANCED EXPRESSION OF PSP-RELATED TRANSCRIPTS AND INTRANEURONAL  
 CC ACCUMULATION OF PSP-LIKE PROTEINS IN THEIR BRAINS.  
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL: M27190; AAA60546.1; -;  
 CC EMBL: M27189; AAA60545.1; -;  
 CC EMBL: M19633; AAA36558.1; -;  
 CC EMBL: J05412; AAA36559.1; -;  
 CC PIR: A25246; A25246.  
 CC PIR: B28351; B28351.









[illegible]

Query Match 45.0% Score 314.5 DB 13 Length 146;

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OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBL_TaxID=8724;
RN [1]
RP SEQUENCE.
RA MEDLINE-96209990; PubMed-8631868;
RX Kawasaki T., Fujimura Y., Usami Y., Suzuki M., Mura S., Sakurai Y.,
RA Makita K., Tanuchi Y., Hirano K., Tittani K.;
*Complete amino acid sequence and identification of the platelet
RT glycoprotein Ib-binding site of Jararaca GP1b-BP, a snake venom
RL protein isolated from Bothrops jararaca.
DR J. Biol. Chem. 271:10635-10639 (1996).
DR HSSP; P23806; I1XX.
DR InterPro: IPR001304; lectin_c.
DR SMART: SM00034; CLECTIN_1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 146 AA; 16720 MW; E28FDEBEF922004 CRC64;

Query Match 48.9% Score 342; DB 13 Length 142;
Best Local Similarity 47.1% Pred. No. 1.6e-30;
Matches 65; Conservative 25; Mismatches 34; Indels 14; Gaps 3;

QY 3 ECPSGWSSYDRCYCKPKQEWNTW----ADAQRCFSEQAKGGHLSVETALASFYDNL 57
Db 5 ECPSDWTHRQYCYKFPQKESMDRSEVDARFCEQAKGGHLSIESDEADFAQLV 64
QY 58 YAKKEYLTRITWIGLRVONKQGPC-----SSISYENYV--DPECFMYSRPTRLREWF 108
Db 65 APIPGSKYIVWIGLRLENKKQCCSSKMSDYSSVSTENLRGNVKKCFALDKQGFRRKW 124
QY 109 KVDCEQDQSFICKETRRP 126
Db 125 NIDCVENGFVCKFIRPR 142

RESULT 4
Q98UJ0 PRELIMINARY; PRT; 146 AA.
AC 098UJ0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FACTOR XI/FACTOR X BINDING PROTEIN A CHAIN.
GN XI/XBP-A.
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OX Viperidae; Crotalinae; Trimeresurus.
OX NCBL_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=VENOME GLAND;
RC Tani A., Ogawa T., Nose T., Nikandorov N.N., Deshmarnu M., Chijiwa T.,
RA Chang C., Fukunaki Y., Ohno M.;
*Characterization and molecular evolution of an anticoagulant protein
RT from Agkistrodon actus venom.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
EMBL AB046491; BAB21452.1; -.
DR HSSP; P23806; I1XX.
DR InterPro: IPR001304; lectin_c.
DR InterPro: IPR003990; pancreatitis_assoc.
DR Pfam: PF000059; lectin_c; 1.
DR PRINTS; PR01504; PNCREATTTSAP.
DR SMART; SM00034; CLECT_1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 146 AA; 16461 MW; 6ADF0E032544316C CRC64;
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OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Deinagkistrodon.  
 OX NCBI\_TaxID=36307;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=VENOM;  
 RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,  
 RA Liu J.;  
 RT "Aggiscutacin, a new fibrinolytic & anti-platelet protein from  
 RT Agkistrodon acutus venom.";  
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF176421; AAF26287.1; -  
 DR HSSP: P23807; I1XX.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 DR SEQUENCE 146 AA; 16726 MW; 7360B6D6864131BB CRC64;

Query Match 37.4%; Score 261.5; DB 13; Length 146;  
 Best Local Similarity 43.2%; Pred. No. 1.7e-21;  
 Matches 54; Conservative 21; Mismatches 41; Indels 9; Gaps 5;

OY 3 ECPGSSSYDRCYKPFQEMTWADQRCSEQAKGHLSTALEAFVNDVLYANKE 62  
 DB 24 DCPSSWSYEGHCYKPFQEMTWADQRCSEQAKGHLSTALEAFVNDVLYANKE 81  
 OY 63 YLTRYTWIGLR-VON-----KGPCSSISENLVDPEFCFVNSRDTLRLEWFKVDCQOHS 117  
 DB 82 LKTDLWIGLKNINCGKWKMSDGTLDYKDMREQFEC-LVSR-TYNNENLSMDCGTTCS 139  
 OY 118 FICKF 122  
 DB 140 FVCKF 144

RESULT 11  
 OY 093427 PRELIMINARY; PRT; 148 AA.  
 AC 093427;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CONVULXIN BETA PRECURSOR.  
 GN CYN BETA.  
 OS Crotalus durissus terrificus (South American rattlesnake).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Crotalus.  
 OX NCBI\_TaxID=8732;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 24-53; 99-109 AND 126-145.  
 RC TISSUE=VENOM GLAND;  
 RX MEDLINE=98524901; PubMed-9657980;  
 RA Leduc M., Bon C.;  
 RT "Cloning of subunits of convulxin, a collagen-like platelet-  
 RT aggregating protein from Crotalus durissus terrificus venom.";  
 RL Biochem. J. 333:389-393(1998).  
 CC -1- FUNCTION: BINDS TO THE PLATELET AND COLLAGEN RECEPTOR,  
 CC GLYCOPROTEIN VI (GPVI).  
 CC -1- SUBUNIT: HETEROHETEROMER OF THREE ALPHA CHAINS AND THREE BETA  
 CC CHAINS.  
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE C-TYPE LECTIN FAMILY.  
 DR EMBL: Y16349; CAA76182.1; -  
 DR HSSP: P23807; I1XX.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS00615; C\_TYPE\_LLECTIN\_1; 1.

DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Venom; Lectin; Glycoprotein; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 148  
 FT DOMAIN 26 146  
 FT DISULFID 26 26  
 FT DISULFID 27 38  
 FT DISULFID 55 144  
 FT DISULFID 100 100  
 FT DISULFID 121 136  
 FT SEQUENCE 148 AA; 17402 MW; 94D7E3E1BC6539BF CRC64;

Query Match 37.4%; Score 261.5; DB 13; Length 148;  
 Best Local Similarity 42.1%; Pred. No. 1.7e-21;  
 Matches 53; Conservative 18; Mismatches 42; Indels 13; Gaps 5;

OY 4 CPGSSSYDRCYKPFQEMTWADQRCSEQAKGHLSTALEAFVNDVLYANKE 63  
 DB 27 CPGSSSYDRCYKPFQEMTWADQRCSEQAKGHLSTALEAFVNDVLYANKE 84  
 OY 64 LTRITWIGLRVONKGPC-----SSISENLVDPEFCFVNSRDTLRLEWFKVDCQOHS 116  
 DB 85 KSTFWIGL--ANNIMNCKMGMQSDGTREKWEHEFEC-LISR-TFDNOMLSARCSDTY 140  
 OY 117 SFICKF 122  
 DB 141 SFVCKF 146

RESULT 12  
 OY 093427 PRELIMINARY; PRT; 135 AA.  
 AC 093427;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE AGGISCUTACIN A CHAIN.  
 OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Deinagkistrodon.  
 OX NCBI\_TaxID=36307;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=VENOM;  
 RA Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,  
 RA Liu J.;  
 RT "Aggiscutacin, a new fibrinolytic & anti-platelet protein from  
 RT Agkistrodon acutus venom.";  
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF176420; AAF26286.1; -  
 DR HSSP: P23806; I1XX.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 DR SEQUENCE 135 AA; 15041 MW; F9A55A3802AFA291 CRC64;

Query Match 37.3%; Score 260.5; DB 13; Length 135;  
 Best Local Similarity 49.0%; Pred. No. 1.9e-21;  
 Matches 47; Conservative 19; Mismatches 23; Indels 7; Gaps 1;  
 OY 3 ECPGSSSYDRCYKPFQEMTWADQRCSEQAKGHLSTALEAFVNDVLYANKE 62  
 DB 24 DCPSSWSYEGHCYKPFQEMTWADQRCSEQAKGHLSTALEAFVNDVLYANKE 83  
 OY 63 YLTRITWIGLRVONKGPC-----SSISENLVD 91  
 DB 84 SAKITWIGLRONKKEKCSIEWSDGSSISENLWIE 119

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RESULT 13
O9PSM9 PRELIMINARY; PRT; 131 AA.
ID 09PSM9:
AC 09PSM9:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE ECLV IX/X-BP ALPHA SUBUNIT=COAGULATION FACTOR IX/FACTOR X-BINDING
DE PROTEIN ALPHA SUBUNIT.
DE ECHIS carinatus (Saw-scaled viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Echis.
NCBI_TaxID=40353;
RN NCB1
RP SEQUENCE.
RX MEDLINE=96196635; PubMed=8611513;
RA Chen Y.L., Tsai I.H.;
RT "Functional and sequence characterization of coagulation factor
RT IX/factor X-binding protein from the venom of Echis carinatus
RT leucogaster."
RL Biochemistry 35:5264-5271(1996).
DR HSP; P23806; IXX.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PR00059; lectin_c; 1.
DR SMART; SM00034; CLECT-1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ SEQUENCE 131 AA; 15439 MW; B85E6C5CBF317E24 CRC64;

Query Match 35.0%; Score 244.5; DB 13; Length 131;
Best Local Similarity 34.6%; Pred. No. 1.1e-19;
Matches 45; Conservative 27; Mismatches 47; Indels 11; Gaps 3;

OY 3 ECPSGSSSYDRYCYKPKFQEMTWADQRFCSQAKGHLSEVTALEASFVNDVLYANKE 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DCLPGMSHGHCHCKYKFNEXKTKMDAERFKLQPKHSLVFSQSAEADVF--VKLTRR 60
OY 61 KELTRYIWIGLRVQNKQPC-----ISYE--NLVDPECFMVSRTLRLEMFKYDC 111
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 KSHSIDPVMWGLTYKGRWKQCSSEMSDGSKITRYQKWKQKQPKCLGLEKQTEPRKWNLY 120
OY 112 CEOQHSFICK 121
   ||: ||:
DB 121 CEERQRTCE 130

RESULT 14
O9I840 PRELIMINARY; PRT; 146 AA.
ID 09I840:
AC 09I840:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AGGRETIN BETA CHAIN (FRAGMENT).
DE Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Calloselasma.
NCBI_TaxID=8717;
RN NCB1
RP SEQUENCE FROM N.A.
RX MEDLINE=9443731; PubMed=10512747;
RA Chung C.H., Au L.C., Huang T.F.;
RT "Molecular cloning and sequence analysis of aggretin, a collagen-like
RT platelet aggregation inducer."
RL Biochem. Biophys. Res. Commun. 263:723-727(1999).
RN RP SEQUENCE FROM N.A.

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RC TISSUE=VENOM GLAND;
RA Chung C.H., Au L.C., Huang T.F.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF244901; AAF79953.1; -.
DR HSSP; P23807; IXX.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PR00059; lectin_c; 1.
DR SMART; SM00034; CLECT-1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
FT NON_TER 146
SQ SEQUENCE 146 AA; 16770 MW; 930839140CFD8908 CRC64;

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Query Match 34.0%; Score 237.5; DB 13; Length 146;
Best Local Similarity 38.6%; Pred. No. 7.9e-19;
Matches 49; Conservative 19; Mismatches 46; Indels 13; Gaps 5;

OY 3 ECPSGSSSYDRYCYKPKFQEMTWADQRFCSQAKGHLSEVTALEASFVNDVLYANKE 62
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 24 DCPGMSHGHCHCKYKFNEXKTKMDAERFKLQPKHSLVFSQSAEADVF--VKLTRR 81
OY 63 YLTRYIWIGLRVQNKQPC-----SSISYENLVDPFECFMVSRTLRLEMFKYDC 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 82 LKANLVMWGL--SNIMGCGNQMWDGARLNYKQWQSEEC-LAFRGVH-TWMLNDCSST 137
OY 116 HSFICKF 122
   ||: ||:
DB 138 CSFICKF 144

RESULT 15
O90WL9 PRELIMINARY; PRT; 124 AA.
ID 090WL9:
AC 090WL9:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AKITONIN (FRAGMENT).
OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Deinagkistrodon.
NCBI_TaxID=36307;
RN NCB1
RP SEQUENCE FROM N.A.
RA Zha X.D., Xu K.S.;
RT "An Anticoagulant Protein From Venom of Agkistrodon acutus."
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF387100; AAK69351.1; -.
FT NON_TER 1
SQ SEQUENCE 124 AA; 14658 MW; 38D3F0BFE3AA0AFC CRC64;

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Query Match 32.8%; Score 229.5; DB 13; Length 124;
Best Local Similarity 39.7%; Pred. No. 5.1e-18;
Matches 50; Conservative 24; Mismatches 43; Indels 9; Gaps 5;

OY 2 LECPGSSSYDRYCYKPKFQEMTWADQRFCSQAKGHLSEVTALEASFVNDVLYANKE 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDCPSDMSSEYGCNYLVVKEKKTMAEAKFCTEQRKECHLVFSHAEVEYFVSKTFPI 60
OY 62 EYLTRYIWIGLR--VQN-----RGQPCSSISYENLVDPFECFMVSRTLRLEMFKYDC 116
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 SY--DLVWIGLKNIMWNGCYKRWKSDGKLDYKDWREQFIC-LVSR-TVNNEMLSMDCGTT 116
OY 117 SFICKF 122
   ||: ||:
DB 117 SFVCEF 122

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Search completed: October 3, 2002, 16:28:44

• Fri Oct 4 08:20:13 2002

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